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OM protein - protein search, using sw model

Run on: June 1, 2004, 15:16:10 ; Search time 22 seconds

(without alignments)
840.095 Million cell updates/sec

Title: US-09-464-685-1

Perfect score: 1874
Sequence: 1 MGFLTLAKLNNELHGOES.....RSLQSVRSEVRIYDYTDV 358Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1846	98.5	358	3	US-08-988-876-3
2	1846	98.5	358	4	US-09-919-172-22
3	768.5	41.0	338	3	US-08-988-876-8
4	768.5	41.0	338	3	US-09-303-524A-2
5	762.5	40.7	325	2	US-08-467-946A-29
6	762.5	40.7	325	2	US-08-467-947A-29
7	694.5	37.1	342	3	US-08-852-824-2
8	694.5	36.8	333	3	US-09-221-456-2
9	690.5	36.8	333	4	US-09-558-740-2
10	668.5	35.7	333	2	US-08-812-871-1
11	466	24.9	293	2	US-08-467-946A-6
12	466	24.9	293	3	US-08-467-947A-6
13	420.5	22.4	319	1	US-08-702-344-28
14	375.5	20.0	342	4	US-08-988-876-9
15	372	19.9	346	4	US-09-585-876-2
16	368.5	19.7	408	2	US-08-742-440A-6
17	360	19.2	326	1	US-08-118-270-39
18	360	19.2	326	5	PCT-US93-08528-39
19	360	19.2	339	4	US-09-170-496D-182
20	357	19.1	339	4	US-08-153-848-44
21	357	19.1	339	2	US-08-812-871-3
22	357	19.1	339	3	US-09-289-843A-44
23	357	19.1	339	4	US-09-088-337B-44
24	357	19.1	339	4	US-09-170-496D-32
25	357	19.1	339	5	PCT-US93-11153-44
26	357	19.1	339	5	PCT-US95-07180-2
27	350	18.7	395	1	US-08-097-938-5

28	350	18.7	395	1	US-08-476-000-5	Sequence 5, Appli
29	350	18.7	395	1	US-08-472-840-5	Sequence 5, Appli
30	350	18.7	395	2	US-08-476-976-5	Sequence 5, Appli
31	350	18.7	395	3	US-08-474-410-5	Sequence 5, Appli
32	350	18.7	398	1	US-08-097-938-6	Sequence 6, Appli
33	350	18.7	398	1	US-08-476-000-6	Sequence 6, Appli
34	350	18.7	398	1	US-08-472-840-6	Sequence 6, Appli
35	350	18.7	398	2	US-08-476-976-6	Sequence 6, Appli
36	350	18.7	398	3	US-08-474-410-6	Sequence 6, Appli
37	350	18.7	398	3	US-08-486-673B-6	Sequence 6, Appli
38	349	18.6	395	3	US-08-486-673B-2	Sequence 2, Appli
39	349	18.6	395	3	US-08-486-673B-5	Sequence 5, Appli
40	349	18.6	399	1	US-08-476-000-61	Sequence 61, Appli
41	349	18.6	399	1	US-08-472-840-61	Sequence 61, Appli
42	349	18.6	399	2	US-08-476-976-61	Sequence 61, Appli
43	349	18.6	399	3	US-08-474-410-61	Sequence 61, Appli
44	349	18.6	399	3	US-08-486-673B-61	Sequence 61, Appli
45	348	18.6	361	4	US-09-170-496D-206	Sequence 206, App

ALIGNMENTS

RESULT 1
US-08-988-876-3
Sequence 3, Application US/08988876

Patent No. 6063596

GENERAL INFORMATION:

APPLICANT: Lal, Preeti

APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED

NUMBER OF SEQUENCES: 9

TITLE OF INVENTION: WITH IMMUNE RESPONSE

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/988,876

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0441 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO. 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 358 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: PROSTUT09

CLONE: 1650519

US-08-988-876-3

Query Match 98.5%; Score 1846; DB 3; Length 358;
 Best Local Similarity 98.6%; Pred. No. 3.8e-138;
 Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGFNLTLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEFDITVLPVLIIFVASILLN 60
 DB 1 MGFNLTLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEFDITVLPVLIIFVASILLN 60
 QY 61 GLAVMIFPHIRNKTSFIYFKNTIVADLIMLTTPFPRIVHDAGFGPMYFKPILCRYSVL 120
 DB 61 GLAVMIFPHIRNKTSFIYFKNTIVADLIMLTTPFPRIVHDAGFGPMYFKPILCRYSVL 120
 QY 121 FYANMYTSIVFGLISIDRYLKVVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPMIILT 180
 DB 121 FYANMYTSIVFGLISIDRYLKVVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPMIILT 180
 QY 181 NGOPTEDNIHDCSKLSPGVKMTAVTVNSCLFVAVLVILIGCYIAISRVIHKSROF 240
 DB 181 NGOPTEDNIHDCSKLSPGVKMTAVTVNSCLFVAVLVILIGCYIAISRVIHKSROF 240
 QY 241 ISOSSRKRKKNOSIRVVAVFTCPYPHLCRIPTFESHDLRLDESACKILYYCKEITL 300
 DB 241 ISOSSRKRKKNOSIRVVAVFTCPYPHLCRIPTFESHDLRLDESACKILYYCKEITL 300
 QY 301 FLSACNVCLDPIIYFPMCRSPSRRLPKKSNIPTRSSISRSLOSVRSEVRITYDYTDV 358
 DB 301 FLSACNVCLDPIIYFPMCRSPSRRLPKKSNIPTRSSISRSLOSVRSEVRITYDYTDV 358

RESULT 2

US-09-919-172-22
 / Sequence 22, Application US/09919172
 / Patent No. 6673545
 / GENERAL INFORMATION:
 / APPLICANT: Farris, Mary
 / TITLE OF INVENTION: PROSTATE CANCER MARKERS
 / FILE REFERENCE: PA-0036 US
 / CURRENT APPLICATION NUMBER: US/09/919,172
 / CURRENT FILING DATE: 2001-07-30
 / PRIOR APPLICATION NUMBER: 60/222,469
 / PRIOR FILING DATE: 2000-07-28
 / NUMBER OF SEQ ID NOS: 102
 / SOFTWARE: PERL Program
 / SEQ ID NO 22
 / LENGTH: 358
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc.feature
 / OTHER INFORMATION: Incyte ID No. 6673545 1650519CD1
 US-09-919-172-22

Query Match 98.5%; Score 1846; DB 4; Length 358;
 Best Local Similarity 98.6%; Pred. No. 3.8e-138;
 Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGFNLTLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEFDITVLPVLIIFVASILLN 60
 DB 1 MGFNLTLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEFDITVLPVLIIFVASILLN 60
 QY 61 GLAVMIFPHIRNKTSFIYFKNTIVADLIMLTTPFPRIVHDAGFGPMYFKPILCRYSVL 120
 DB 61 GLAVMIFPHIRNKTSFIYFKNTIVADLIMLTTPFPRIVHDAGFGPMYFKPILCRYSVL 120
 QY 121 FYANMYTSIVFGLISIDRYLKVVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPMIILT 180
 DB 121 FYANMYTSIVFGLISIDRYLKVVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPMIILT 180
 QY 181 NGOPTEDNIHDCSKLSPGVKMTAVTVNSCLFVAVLVILIGCYIAISRVIHKSROF 240
 DB 181 NGOPTEDNIHDCSKLSPGVKMTAVTVNSCLFVAVLVILIGCYIAISRVIHKSROF 240

QY 241 ISOSSRKRKKNOSIRVVAVFTCPYPHLCRIPTFESHDLRLDESACKILYYCKEITL 300
 DB 241 ISOSSRKRKKNOSIRVVAVFTCPYPHLCRIPTFESHDLRLDESACKILYYCKEITL 300
 QY 301 FLSACNVCLDPIIYFPMCRSPSRRLPKKSNIPTRSSISRSLOSVRSEVRITYDYTDV 358
 DB 301 FLSACNVCLDPIIYFPMCRSPSRRLPKKSNIPTRSSISRSLOSVRSEVRITYDYTDV 358

RESULT 3

US-08-988-876-8
 / Sequence 8, Application US/08988876
 / Patent No. 6063596
 / GENERAL INFORMATION:
 / APPLICANT: Lal, Preeti
 / APPLICANT: Bandman, Olga
 / APPLICANT: Hillman, Jennifer L.
 / APPLICANT: Yue, Henry
 / TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
 / TITLE OF INVENTION: WITH IMMUNE RESPONSE
 / NUMBER OF SEQUENCES: 9
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Incyte Pharmaceuticals, Inc.
 / STREET: 3174 Porter Drive
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94304
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FastSeq for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/988,876
 / FILING DATE: Herewith
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Billings, Lucy J.
 / REGISTRATION NUMBER: 36,749
 / REFERENCE/DOCKET NUMBER: PF-0441 US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 650-855-0555
 / TELEFAX: 650-845-4166
 / TELEX:
 / INFORMATION FOR SEQ ID NO: 8:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 338 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / IMMEDIATE SOURCE:
 / LIBRARY: Genbank
 / CLONE: 285995
 US-08-988-876-8

Query Match 41.0%; Score 768.5; DB 3; Length 338;
 Best Local Similarity 47.6%; Pred. No. 2.9e-53;
 Matches 147; Conservative 64; Mismatches 97; Indels 1; Gaps 1;

QY 44 VLPLVLIIFVASILLNGLAVMIFPHIRNKTSFIYFKNTIVADLIMLTTPFPRIVHDAG 103
 DB 24 IIVPLVCMVFIADILNGVSGWIFVYPSKSTIYFKNTIVADLIMLTTPFPRIVHDAG 83
 QY 104 FGPWFYFKILCRYSVLFYANMYTSIVFGLISIDRYLKVVKPFGDSRMYSITFTKVL 163
 DB 84 LGMWQNLVFCRISAVLFTVMYVSVIFPGILSFDYIKIVKPLMTSIFQSVYSGLASV 143
 QY 164 CWMVIAVLSLEPIIITNGOPTEDNIHDCSKLSPGVKMTAVTVNSCLFVAVLVILIG 223
 DB 164 CWMVIAVLSLEPIIITNGOPTEDNIHDCSKLSPGVKMTAVTVNSCLFVAVLVILIG 223

Db 144 IVMMLMLLAVPNILITNQSREVTQIKCIELKSELGRMKHASNIFVAFIWFILLLI 203
Qy 224 GCYIAISRYIHKS-RQFISOSRRKKNOSIRVVAVFCTCFLPYHLCRIPFTSHDR 282
Db 204 VFTYATITKKIFKSHLKSRSNSTSVKKSRSNIFSIVPFVCFVPHIARIITYTSQTEA 263
Qy 283 LIDESAQILYYCKEITLFLSACNVCDDPIIYFPMCRSFRLLFKKSNIRTSSESIRSIQ 342
Db 264 HYSQSKELIRYMKFTLLLSAANCDDPIIYFPLQCPREILCKKHLPLKAQNDLDS 323
Qy 343 SVRSEVR 351
Db 324 RIKRGNTTL 332

RESULT 4
US-09-303-524A-2
Sequence 2, Application US/09303524A
Patent No. 6238873
GENERAL INFORMATION:
APPLICANT: CHAMBERS, JONATHAN K.
APPLICANT: STEWART, BRIAN R.
APPLICANT: AMES, ROBERT S.
APPLICANT: SARAU, HENRY M.
APPLICANT: FOLEY, JIM
APPLICANT: ARNOLD, ANNE ROMANIC
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
FILE REFERENCE: GP50007
CURRENT APPLICATION NUMBER: US/09/303,524A
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,957
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 2
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-09-303-524A-2

Query Match 41.0%; Score 768.5; DB 3; Length 338;
Best Local Similarity 47.6%; Pred. No. 2,9e-53;
Matches 147; Conservative 64; Mismatches 97; Indels 1; Gaps 1;
Qy 44 VLPVYLIIFFVASILNGLAWIFPHIRKTSFIYLNKNIIVADDIMTLTTPPRIVHDAG 103
Db 24 IIPVYKCVFIAGILNLSGWSGIFVYVPSKSFIIYLNKNIIVADVMSTLTPFKILGDSG 83
Qy 104 FGPWFYKFLCRYSVLFPYANNYSIVFLGLISIDRYLKVKVPFGDSRMYSTTFKVLVS 163
Db 84 LGPMQJNFVCRVSAVLFPYVMYVSIIVFGLISPDYKYIVKPLMTSFIQSVSYSKLSV 143
Qy 164 CWMVMAVLSLPIIITLNGOPTEDNIHDSKLSPLGVKMHNAVYVNSCLFVAVLVILI 223
Db 144 IVMMLMLLAVPNILITNQSREVTQIKCIELKSELGRMKHASNIFVAFIWFILLLI 203
Qy 224 GCYIAISRYIHKS-RQFISOSRRKKNOSIRVVAVFCTCFLPYHLCRIPFTSHDR 282
Db 204 VFTYATITKKIFKSHLKSRSNSTSVKKSRSNIFSIVPFVCFVPHIARIITYTSQTEA 263
Qy 283 LIDESAQILYYCKEITLFLSACNVCDDPIIYFPMCRSFRLLFKKSNIRTSSESIRSIQ 342
Db 264 HYSQSKELIRYMKFTLLLSAANCDDPIIYFPLQCPREILCKKHLPLKAQNDLDS 323
Qy 343 SVRSEVR 351
Db 324 RIKRGNTTL 332

RESULT 5

US-08-467-948A-29
Sequence 29, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-29

Query Match 40.7%; Score 762.5; DB 2; Length 325;
Best Local Similarity 48.2%; Pred. No. 8,4e-53;
Matches 146; Conservative 63; Mismatches 93; Indels 1; Gaps 1;
Qy 44 VLPVYLIIFFVASILNGLAWIFPHIRKTSFIYLNKNIIVADDIMTLTTPPRIVHDAG 103
Db 23 IIPVYKCVFIAGILNLSGWSGIFVYVPSKSFIIYLNKNIIVADVMSTLTPFKILGDSG 82
Qy 104 FGPWFYKFLCRYSVLFPYANNYSIVFLGLISIDRYLKVKVPFGDSRMYSTTFKVLVS 163
Db 83 LGPMQJNFVCRVSAVLFPYVMYVSIIVFGLISPDYKYIVKPLMTSFIQSVSYSKLSV 142
Qy 164 CWMVMAVLSLPIIITLNGOPTEDNIHDSKLSPLGVKMHNAVYVNSCLFVAVLVILI 223
Db 144 IVMMLMLLAVPNILITNQSREVTQIKCIELKSELGRMKHASNIFVAFIWFILLLI 202
Qy 224 GCYIAISRYIHKS-RQFISOSRRKKNOSIRVVAVFCTCFLPYHLCRIPFTSHDR 282
Db 203 VFTYATITKKIFKSHLKSRSNSTSVKKSRSNIFSIVPFVCFVPHIARIITYTSQTEA 262
Qy 283 LIDESAQILYYCKEITLFLSACNVCDDPIIYFPMCRSFRLLFKKSNIRTSSESIRSIQ 342
Db 263 HYSQSKELIRYMKFTLLLSAANCDDPIIYFPLQCPREILCKKHLPLKAQNDLDS 322

QY 343 SVR 345
Db 323 RIK 325

RESULT 6

US-08-467-947A-29
; Sequence 29, Application US/08467947A
; Patent No. 6090575
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR1
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,947A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEPPER, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-467-947A-29

Query Match 40.7%; Score 762.5; DB 3; Length 325;
Best Local Similarity 48.2%; Pred. No. 8.4e-53;
Matches 146; Conservative 63; Mismatches 93; Indels 1; Gaps 1;

QY 44 VLPVYLIIFVAVSIILNGIAWIFPHINKTSFIYLYKNIVVADLIMLTTPPRIVHDAG 103
Db 23 IIPVLYCWFAGIILNGVSGWIFYPVPSKSFIIYLNKIVADPVMSTLTPFKILGDSG 82
QY 104 FGPWFKFLCRYSVLFFANNYTSIVFLGLISIDRYLKVVPFGDSMWYSITPFKVLSV 163
Db 83 LGPWQANFVCRVSAVLFFVANNYTSIVFLGLISIDRYLKVVPFGDSMWYSITPFKVLSV 142
QY 164 CVMVMAVLSPLNIIITNGQPTEDNIHDCSKLSPGVKMTAVTVYVNSCLFVAVLVILI 223
Db 143 IVMMLLAVVNIILITNQSVEVTVQIKCIELKSELGKMKHAKSYIVAVIFWLVFILLI 202
QY 224 GCYIAISYVHKSS-RQFISQSSRRKKNQSRVAVVAFPCFLPYHLCRIPTFFSHLDR 282

Db 203 VEPYATITKKIFKSHLKSSRNSTSVKKSNNIFSIYFVPCVFPYHARIPIYTSQTEA 262
QY 283 LIDESAQKILYCKEITLFLSACVNCUDPPIYFFWCRESRRLFKSNIRRSISRLQ 342
Db 263 HYSQSKETILRYMKEFTLLSNANVCUDPPIYFFWCQFRELCKKHLPIKAQNDLDS 322
QY 343 SVR 345
Db 323 RIK 325

RESULT 7

US-08-852-824-2
; Sequence 2, Application US/08852824C
; Patent No. 6060272
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488.1220000
; CURRENT APPLICATION NUMBER: US/08/852,824C
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: genomic
US-08-852-824-2

Query Match 37.1%; Score 694.5; DB 3; Length 342;
Best Local Similarity 42.2%; Pred. No. 2e-47;
Matches 139; Conservative 68; Mismatches 113; Indels 9; Gaps 5;

QY 25 NRSQPGKNITL--HNEEDTIVLPVLYLIIFVASIILNGIAWIFPHINKTSFIYLYK 81
Db 6 NLTSPAG-NISLCTRDYKITQVLPFLYTVLFVGLITNGLAMRIFQIRSKSNFIIFLK 64
QY 82 NIVVADLIMLTTPPRIVHDAGRGPWFKFLCRYSVLFFANNYTSIVFLGLISIDRYL 141
Db 65 NTVISDLMLITFPFKILSDKLGCTGPLRTFVCQVTSIVIFFTWYISISFLGLITDYO 124
QY 142 KVPKFGDSRWYSITPFKVLSCVAVIMAVLSPLNIIITNGQPTEDNIHDCSKLSPGV 201
Db 125 KTRPFPKTSNPKNLGAKILSVIWMFPLSLPMLITRQRPDKVKKCSFLKSEFGL 184
QY 202 KMTAVTVYVNSCLFVAVLVILIGCYIAISRYHKS--SRQFISQSSRRKKNQSRVVA 259
Db 185 VMHEIVNYICQVIMINFLIYVICYTLITKELYSYVTRGVGKVPK-KVNVAVFIIA 243
QY 260 VFTCPFLPYHLCRIPTFFSHLDRLLDESQKILYCKEITLFLSACVNCUDPPIYFPCR 319
Db 244 VFICFVFPFHARIPYTLSCQDVDFCTAENTLIFYVESTLMTLSNACDPLFIYFPLCK 303
QY 320 SFSRRLFKSNIRRSISRLQSVRSE 348
Db 304 SFRNSLI--SWLKCPNATSLSDQNRKKE 330

RESULT 8

US-09-221-456-2
; Sequence 2, Application US/09221456
; Patent No. 6162899
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HAUSEY, WENDY
; APPLICANT: MUIR, ALISON
; APPLICANT: CHAMBERS, JON
; APPLICANT: SZEKERES, PHILIP
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
; TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEA81 RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia

STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,456
FILING DATE: 28-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,975
FILING DATE: 23-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70318-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-221-456-2

Query Match 36.8%; Score 690.5; DB 3; Length 333;
Best Local Similarity 41.1%; Pred. No. 4.1e-47;
Matches 127; Conservative 66; Mismatches 97; Indels 19; Gaps 4;

QY 33 NTTLHNEF-----DT----YLPVLYLIIFVASILLNGLAWIFPHINKTSFIYYL 80
DB 2 NTTWOGFNRSERCPRDRIYQVLPALYTVFPLTGILLNTLALWVFWHIPSSSTFIYYL 61
QY 81 KNIVADLIMLTLPFRIVHDAGFGPMYFKFLGRYSVLFPANNYSIVFLGISIDRY 140
DB 62 KNTLVADLIMLTLPFKILSDSHLAPWOLRAVFCFSSVIFETWVGIVLGLIAFRF 121
QY 141 LKVVKPFGRSRYSTFTFKVLSCVWVIMAVLSLNNILTNQOPTEDNIDHCSKLSPG 200
DB 122 LKIRPLRNIFLKKPFAKTVSIFWFLPFLISLNTLSKENTPSSVKKASLKGKPLG 181
QY 201 VKHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSROFISQSRKKNQSR----V 256
DB 182 LKHWQMVNNICQFIWTFVFIIMLVFYVVIYAKKYDSYRK--SKSKDKNNKKLEGKVFV 238
QY 257 VVAVFPFCPLPYHLCRIPTFSHLDRLLDESAOKILYYCKEITFLSACVCLDPIIYF 316
DB 239 VVAVFPFCFAPHRARVPYTHSQTNKTKDCLQNLQFLAKETTLFLAATNICMDPLIYF 298
QY 317 MCRSFSRRL 325
DB 299 LCKKFTKTL 307

RESULT 9
US-09-558-740-2
Sequence 2, Application US/09558740
Patent No. 6358695
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HAUSEY, WENDY
APPLICANT: MUIR, ALISON
APPLICANT: CHAMBERS, JON
APPLICANT: SZEKERS, PHILIP

TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE HNEAA81 RECEPTOR
FILE REFERENCE: GH-70318-2
CURRENT APPLICATION NUMBER: US/09/558,740
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 08/956,975
PRIOR FILING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: 09/221,456
PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 333
TYPE: PR
ORGANISM: HOMO SAPIENS
US-09-558-740-2

Query Match 36.8%; Score 690.5; DB 4; Length 333;
Best Local Similarity 41.1%; Pred. No. 4.1e-47;
Matches 127; Conservative 66; Mismatches 97; Indels 19; Gaps 4;

QY 33 NTTLHNEF-----DT----YLPVLYLIIFVASILLNGLAWIFPHINKTSFIYYL 80
DB 2 NTTWOGFNRSERCPRDRIYQVLPALYTVFPLTGILLNTLALWVFWHIPSSSTFIYYL 61
QY 81 KNIVADLIMLTLPFRIVHDAGFGPMYFKFLGRYSVLFPANNYSIVFLGISIDRY 140
DB 62 KNTLVADLIMLTLPFKILSDSHLAPWOLRAVFCFSSVIFETWVGIVLGLIAFRF 121
QY 141 LKVVKPFGRSRYSTFTFKVLSCVWVIMAVLSLNNILTNQOPTEDNIDHCSKLSPG 200
DB 122 LKIRPLRNIFLKKPFAKTVSIFWFLPFLISLNTLSKENTPSSVKKASLKGKPLG 181
QY 201 VKHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKSROFISQSRKKNQSR----V 256
DB 182 LKHWQMVNNICQFIWTFVFIIMLVFYVVIYAKKYDSYRK--SKSKDKNNKKLEGKVFV 238
QY 257 VVAVFPFCPLPYHLCRIPTFSHLDRLLDESAOKILYYCKEITFLSACVCLDPIIYF 316
DB 239 VVAVFPFCFAPHRARVPYTHSQTNKTKDCLQNLQFLAKETTLFLAATNICMDPLIYF 298
QY 317 MCRSFSRRL 325
DB 299 LCKKFTKTL 307

RESULT 10
US-08-812-871-1
Sequence 1, Application US/08812871
Patent No. 5955303
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0237 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 333 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: MMLR3DT01
 CLONE: 568987
 US-08-812-871-1

Query Match 35.7%; Score 668.5; DB 2; Length 333;
 Best Local Similarity 40.1%; Pred. No. 2.2e-45;
 Matches 124; Conservative 67; Mismatches 99; Indels 19; Gaps 4;

33 NTTLHNEF-----DT-----IVLPVYLIIIVASIIINGLAWIIFPHIRKTSIFLYL 80
 2 NTTWGSGFRNSRCPDTRIVQLVFPALTYVFTGLTLNTLAWVFIHPSSTFIYL 61
 81 KNIVADLIMTLTPFRIYHDAGFGPWYFKILCRYSVLFYANMTSYVFLGLISIDRY 140
 62 KNTLVADLIMTLMLPKILSDSHLAPWQRAFCVCRSSVIFETWVGIVLGLIAFDRF 121
 141 LKVVKPGDSRMYSITFTKLVSCVWVYNAVLSLPIILITNGOPTEDNHDCKSLSPG 200
 122 LKIRPLRNIPLKPPWGVKTVSIFIFWFFISLPMILSNKEATPSSVKKCASLKGPIV 181
 201 VKMHTAVTVNSCLFPAVLVILIGCYIAISRYIHKSRSQFISSSRKREHNSIR----V 256
 182 LKHQWVNNICQFIPTVILMLVFPVYIAKVYDSYRK---SKCKDRKAKKLGKVPV 238
 257 VVAVPTFCPLPYHLCPFTFESHLDRLDESQKILYCKEITFLSACNVCLEPIYFF 316
 239 VVPEVFCFAPHPFARVPYTHSQTNKKTDCRLQNLQFLAKETTLPLAATNICMDPLISIF 298
 317 MCRSFSRRL 325
 299 LCKKTEPKL 307

RESULT 11
 US-08-467-948A-6
 Sequence 6, Application US/08467948A
 Patent No. 5998164
 GENERAL INFORMATION:
 APPLICANT: LI, YI
 APPLICANT: CAO, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 TITLE OF INVENTION: Coupled Receptor GPR2
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNF, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,948A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEPP, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 293 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-467-948A-6

Query Match 24.9%; Score 466; DB 2; Length 293;
 Best Local Similarity 40.3%; Pred. No. 1.8e-29;
 Matches 85; Conservative 47; Mismatches 67; Indels 12; Gaps 2;

33 NTTLHNEF-----DT-----IVLPVYLIIIVASIIINGLAWIIFPHIRKTSIFLYL 80
 2 NTTWGSGFRNSRCPDTRIVQLVFPALTYVFTGLTLNTLAWVFIHPSSTFIYL 61
 81 KNIVADLIMTLTPFRIYHDAGFGPWYFKILCRYSVLFYANMTSYVFLGLISIDRY 140
 62 KNTLVADLIMTLMLPKILSDSHLAPWQRAFCVCRSSVIFETWVGIVLGLIAFDRF 121
 141 LKVVKPGDSRMYSITFTKLVSCVWVYNAVLSLPIILITNGOPTEDNHDCKSLSPG 200
 122 LKIRPLRNIPLKPPWGVKTVSIFIFWFFISLPMILSNKEATPSSVKKCASLKGPIV 181
 201 VKMHTAVTVNSCLFPAVLVILIGCYIAISRYIHKSRSQFISSSRKREHNSIR----V 231
 182 LKHQWVNNICQFIPTVILMLVFPVYIAKVYDSYRK---SKCKDRKAKKLGKVPV 212

RESULT 12
 US-08-467-947A-6
 Sequence 6, Application US/08467947A
 Patent No. 6090575
 GENERAL INFORMATION:
 APPLICANT: LI, YI
 APPLICANT: CAO, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 TITLE OF INVENTION: Coupled Receptor GPR1
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNF, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA: US/08/467, 947A
APPLICATION NUMBER: US/08/467, 947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2500
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-947A-6

Query Match 24.9%; Score 466; DB 3; Length 293;
Best Local Similarity 40.3%; Pred. No. 1.8e-29;
Matches 85; Conservative 47; Mismatches 67; Indels 12; Gaps 2;

QY 33 NTLTNEP-----DT-----YLPVLVLIIPVASILNGLAVWIFPHIRNKTSPIFYL 80
DB 2 NTTWAGNRSRCKPQDTRIVQLVLPALYTVFLGILLTALWVPHISSSTFIYL 61
QY 81 KNIVADILMTLTPPRIVHDAGFGPMYFKFLCYTSVLPFANNYTSIVPLGLISIRY 140
DB 62 KNTLVADILMTLMPFKILSDSHLAPWQLRAFCRPSVIFETWYGVILGLIAPDRF 121
QY 141 LKVVPEGDSRWYSTFTFKVLSVCVWVIMAVLSLPIILITNGOPTEDNIDHCSKLSPG 200
DB 122 LKRIPLNITLKKKRWGKTVSIFWPFWSLSPNMLSKKATPSVKKASLKPGL 181
QY 201 VKMHTAVTVNSCLFVAVLVILIGCYIAISR 231
DB 182 LKMHQMVNNICQFIWTVFILMLVYVVIK 212

RESULT 13
US-08-702-344-28
Sequence 28, Application US/08702344
Patent No. 5723315
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavalley, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,344

FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-344-28

Query Match 22.4%; Score 420.5; DB 1; Length 319;
Best Local Similarity 29.6%; Pred. No. 7.4e-26;
Matches 83; Conservative 64; Mismatches 126; Indels 7; Gaps 3;

QY 49 YLIIFVASILNGLAVWIFPHIR-NKTSPIFYLNIVADILMTLTPPRIVHDAGFGPM 107
DB 21 FYLVFLVGLIGSCFATWAFIQKTNHRCVSIYLLNLTADELTLALPVKIVDLGVAPW 80
QY 108 YFKRILCRYTSVLPFANNYTSIVPLGLISIRYLVKVPFSDSMYSTFTKVLSCVWV 167
DB 81 KLIKFCQVADCLYINMYLSIFLAFVSIIDRLQTHSKYIVIOEDGFMKISTVWL 140
QY 168 IMAVLSLPIILITNGOPTEDNIDHCSKLSPGKVMHTAVTVNSCLFV--AVILIGC 225
DB 141 MVLIMPMMIPIKDIKESNNGCMFKFGKMMHLLTFCVATLANSAILISNC 200
QY 226 YIAISRYIKSSROFISQSRKRNOSIRVAVVFTCLPYHLCAIPTFSHLDRLLD 285
DB 201 LVINQLVRNKNENY---PVKKALINILVTTGYIICFVPHYIVRIPTLSQTEVITD 256
QY 286 ESAQKILYCKEITLFLSACVNCIDPIYFMCSPSRL 325
DB 257 CSTRISLFAKKAETLLAVSNLCEDPIYLHYLSKAFRSKV 296

RESULT 14
US-08-988-876-9
Sequence 9, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Herewith
APPLICATION NUMBER: US/08/988,876
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36, 749
 REFERENCE/DOCKET NUMBER: PF-0441 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 342 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 49443
 US-08-988-876-9

Query Match 20.0%; Score 375.5; DB 3; Length 342;
 Best Local Similarity 27.2%; Pred. No. 2,8e-22;
 Matches 96; Conservative 74; Mismatches 148; Indels 35; Gaps 9;

QY 22 NSGNRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILNGLAVITFPHI--RNKTSFIF 78
 DB 4 NSSRVD-----SEFRYTLFPVYSIIIFVLGINGVYLVFARLPKSKLNEIKI 54
 QY 79 YLKNIVADLIMLTLPFPRIVDHAGCPWYEFKFLCRYSVLFPYANMTSIVFLGLISTD 138
 DB 55 FFWNLTVADLFLITLPLMWIVYSSNQNMFLPKPLNLAGCLFINTYCSVAFGLVITYN 114
 QY 139 RLKLYVKPFGDSRMYSITFTKVLSCVWYIMASL-----VLSLPIIILNGOPTEDNIHD 191
 DB 115 RFOAVKYPFKTQATRRKGIASLVIWAIIVAASVFLWMDSTNVV--SKAGSGNITR 172
 QY 192 GSKLSPGLGVKMTAVTVYNSCL--FVAVLVILIGCYAISRYIHKSRSQPSISQSR-- 246
 DB 173 CREHYE---KSKPLIHIICIVLGFIVFLILFCNVI---IHTLLRQPVKQBNAE 225
 QY 247 -RRKINOSIRVVAVFTFCLPYHLCRIPFTFSHLDRLLDESAQKILYCKEITLPLSAC 305
 DB 226 VRRRALMWCVLAVFVLCFVPHHWQLPWTLAELG-MWPSNNHQAINDAHQVTLCLLT 284
 QY 306 NVCLEPIITFFMCRSFRRLFKKSNIRTPSESIRSLQSVRSSEVRHYDYTDV 358
 DB 285 NCVLPVLYICFLTKRKRLSEKLNIMSSQKSRVTTDTGTGEMALPINHTPV 337

RESULT 15

US-09-585-876-2
 Sequence 2, Application US/09585876
 Patent No. 6586205
 GENERAL INFORMATION:
 APPLICANT: Glucksmann, Maria Alexandra
 APPLICANT: Sillos-Santiago, Immaculada
 TITLE OF INVENTION: 43239, A No. 6586205el GPCK-like Molecule and
 TITLE OF INVENTION: Uses Thereof
 FILE REFERENCE: 5800-88
 CURRENT APPLICATION NUMBER: US/09/585,876
 CURRENT FILING DATE: 2000-06-01
 EARLIER APPLICATION NUMBER: 60/182,061
 EARLIER FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 346
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-585-876-2

Query Match 19.9%; Score 372; DB 4; Length 346;
 Best Local Similarity 28.4%; Pred. No. 5.3e-22;
 Matches 98; Conservative 68; Mismatches 153; Indels 26; Gaps 10;

QY 19 ESHNSGRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILNGLAVITFPHI--RNKTSFIF 77
 DB 16 EMEPNIGTFSNNNSRNTTEN-FKREFFPIYLIIFGVGLNGLSIVFLQPYKKSSTVN 74
 QY 78 YLKNIVADLIMLTLPFPRIVDHAGCPWYEFKFLCRYSVLFPYANMTSIVFLGLISTD 137
 DB 75 VFMLNLASDILLFISTLPPRADYYLRGSSWIFGDLACRIMSYSILYVMYSIYFLTVLSV 134
 QY 138 DRYLKYVKPFGDSRMYSITFTKVLSCVWYIMASL-----VLSLPIIILNGOPTEDNIHDCSLKS 197
 DB 135 VRFLAMVHPFRLHVTISRSAMILCGIITWIMASSI--MLDGSQNGSVTSCLLENL 192
 QY 198 PLGVKMTA--VFVNSCLFVAVLVILIGCYAISRYIHKSRSQPSISQSRKRKNOSIR 255
 DB 193 YKIKLOTMTYIALVGVCLPFFTLST--CYLLIRVLKYE--VPSGLRVSHRKALT 247
 QY 256 VVV--AVFTCLPYHLCRIPFTFSHLDRLLDESAQKILYCKEITLPLSACVCLDPI 312
 DB 248 TIITLIIFFLCFLPYHTLFTVHLTWKVGICKRDLHKALV---ITLVLAANAACFNPL 303
 QY 313 IYFMCRSFSRRLFKKSNIR-----TRSESIRSLQSVRSSEVRHYDYTDV 351
 DB 304 LYFAGNFKDRL--KSLRKGHPOKAKTKCVFPVSWLRKRETRV 346

Search completed: June 1, 2004, 15:19:51
 Job time : 24 sec

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 1, 2004, 15:17:20 ; Search time 48 Seconds

(without alignments)
2082.736 Million cell updates/sec

Title: US-09-464-685-1

1874

Perfect score: 1 MGFNLTLLAKLNNELHGOES.....RSLQSVRSRVRIVYDITDV 358

Sequence:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1874	100.0	358	9	US-09-826-508-10
2	1874	100.0	358	10	US-09-741-783-1
3	1874	100.0	358	12	US-10-165-844-1
4	1874	100.0	358	14	US-10-225-567A-418
5	1874	100.0	358	15	US-10-295-027-1255
6	1874	100.0	358	15	US-10-295-027-1255
7	1874	100.0	358	15	US-10-188-832-135
8	1874	100.0	358	16	US-10-693-605-18
9	1867	99.6	358	9	US-09-919-172-22
10	1846	98.5	358	9	US-09-974-298-86
11	1846	98.5	358	14	US-10-121-101B-1
12	889	47.4	196	15	US-10-264-237-2659
13	768.5	41.0	338	9	US-09-919-497-77
14	768.5	41.0	338	10	US-09-745-842-13
15	768.5	41.0	338	12	US-10-433-146-1

16	768.5	41.0	338	14	US-10-121-101B-10	Sequence 10, Appl
17	768.5	41.0	338	14	US-10-225-567A-213	Sequence 213, App
18	768.5	41.0	338	15	US-10-352-684A-42	Sequence 42, Appl
19	762.5	40.7	325	14	US-10-024-494-29	Sequence 29, Appl
20	742.5	39.6	338	9	US-09-826-508-20	Sequence 20, Appl
21	742.5	39.6	338	12	US-10-433-146-2	Sequence 2, Appl1
22	703.5	37.5	333	14	US-10-189-576-2	Sequence 2, Appl1
23	700.5	37.4	343	10	US-09-745-842-2	Sequence 2, Appl1
24	694.5	37.1	342	9	US-09-835-922-2	Sequence 2, Appl1
25	694.5	37.1	342	9	US-09-827-927A-2	Sequence 2, Appl1
26	694.5	37.1	342	9	US-09-780-576-2	Sequence 2, Appl1
27	694.5	37.1	342	9	US-09-964-008-1	Sequence 1, Appl1
28	694.5	37.1	342	10	US-09-745-842-6	Sequence 6, Appl1
29	694.5	37.1	342	12	US-09-875-076-32	Sequence 32, Appl
30	694.5	37.1	342	12	US-09-876-252-34	Sequence 34, Appl
31	694.5	37.1	342	12	US-10-343-550A-26	Sequence 26, Appl
32	694.5	37.1	342	14	US-10-225-567A-643	Sequence 643, App
33	694.5	37.1	342	14	US-10-333-844-2	Sequence 2, Appl1
34	694.5	37.1	342	14	US-10-272-983-32	Sequence 32, Appl
35	694.5	37.1	342	14	US-10-393-807-32	Sequence 32, Appl
36	694.5	37.1	342	15	US-10-417-820A-34	Sequence 34, Appl
37	692.5	37.0	315	10	US-09-745-842-4	Sequence 4, Appl1
38	692.5	37.0	333	10	US-09-924-125-2	Sequence 2, Appl1
39	692.5	37.0	333	10	US-09-957-187-2	Sequence 2, Appl1
40	692.5	37.0	333	14	US-10-243-106-2	Sequence 2, Appl1
41	692.5	37.0	333	14	US-10-225-567A-514	Sequence 514, App
42	692.5	37.0	333	15	US-10-352-684A-34	Sequence 34, Appl
43	692.5	37.0	333	15	US-10-308-968-2	Sequence 2, Appl1
44	692.5	37.0	333	16	US-10-692-605-8	Sequence 8, Appl1
45	690.5	36.8	333	9	US-09-769-159-2	Sequence 2, Appl1

ALIGNMENTS

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US-09-826-508-10
; Sequence 10, Application US/09826508
; Patent No. US20010025099A1
;
GENERAL INFORMATION:
; APPLICANT: Nabi Elshourbagy
; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
; TITLE OF INVENTION: and Polynucleotides
; FILE REFERENCE: GP-7074AUSB
; CURRENT APPLICATION NUMBER: US/09/826,508
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 358
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-826-508-10
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Query Match 100.0%; Score 1874; DB 9; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.3e-162; Indels 0; Gaps 0;
Matches 358; Conservative 0; Mismatches 0;

QY	1	MGFNTLLAKLNNELHGOES	NSGRSDGPGKNTT	LHNEFDITVL	PVLYLII	FVASILLN	60
DB	1	MGFNTLLAKLNNELHGOES	NSGRSDGPGKNTT	LHNEFDITVL	PVLYLII	FVASILLN	60
QY	61	GLAVIFPHIRKRS	FTYLLKXIVAD	IMLTTPFR	IVHDAGF	PPWPKFLICRYTSVL	120
DB	61	GLAVIFPHIRKRS	FTYLLKXIVAD	IMLTTPFR	IVHDAGF	PPWPKFLICRYTSVL	120
QY	121	FYANNYSIVF	GLISIDRYLK	KVVP	FGDSRMYST	TFKVLSCVWVMAVLSLNIIT	180
DB	121	FYANNYSIVF	GLISIDRYLK	KVVP	FGDSRMYST	TFKVLSCVWVMAVLSLNIIT	180
QY	181	NGOPTEDNIH	DSKLSKSP	LGVMHTAV	TVVNSCLF	VAVLVILIGCYIAISRYHKS	240
DB	181	NGOPTEDNIH	DSKLSKSP	LGVMHTAV	TVVNSCLF	VAVLVILIGCYIAISRYHKS	240

Db 181 NGQPTEDNIDHCSKLSPLGVKMTAVTVVNSCLFVAVVILIGCYIAISRYIHKSROP 240
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Hodge, Martin R.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Weich, Nadine S.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding
; FILE REFERENCE: 35800/248302
; CURRENT APPLICATION NUMBER: US/10/165,844
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 09/088,857
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 09/324,465
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 09/464,685
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/741,783
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/145,745
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: US 09/383,745
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 09/234,923
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: US 09/340,880
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-741-783-1

RESULT 2

US-09-741-783-1
; Sequence 1, Application US/09741783
; Publication No. US20030162172A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Hodge, Martin R.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Weich, Nadine S.
; TITLE OF INVENTION: 2871 RECEPTOR, A NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 35800/207283
; CURRENT APPLICATION NUMBER: US/09/741,783
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/464,685
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 09/324,465
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 09/088,857
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-741-783-1

Query Match 100.0%; Score 1874; DB 10; Length 358;
Best Local Similarity 100.0%; Pred. No. 6,3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNPLTLAKLPNNELHGOESHNSGNRSDGPKNTTLNNEPDTIVLPVYLIIIFVASILLN 60
Db 1 MGNPLTLAKLPNNELHGOESHNSGNRSDGPKNTTLNNEPDTIVLPVYLIIIFVASILLN 60
QY 61 GLAWMIFPHIRNKTSIFLYLKNIVADLIMTLTPPRIVHDAGPGPWYFKFLLCRYSVL 120
Db 61 GLAWMIFPHIRNKTSIFLYLKNIVADLIMTLTPPRIVHDAGPGPWYFKFLLCRYSVL 120
QY 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMTSITFTKVLSCVWVIMAVLSLPIIILT 180
Db 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMTSITFTKVLSCVWVIMAVLSLPIIILT 180
QY 181 NGQPTEDNIDHCSKLSPLGVKMTAVTVVNSCLFVAVVILIGCYIAISRYIHKSROP 240
Db 181 NGQPTEDNIDHCSKLSPLGVKMTAVTVVNSCLFVAVVILIGCYIAISRYIHKSROP 240
QY 241 ISQSRKRKNOSIRVVAVVFTCFPLPYHLCRIPFTSHDRLLDDESAOKILYYCKEITL 300
Db 241 ISQSRKRKNOSIRVVAVVFTCFPLPYHLCRIPFTSHDRLLDDESAOKILYYCKEITL 300
QY 301 FLASACNVCLDPIIYFPMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358
Db 301 FLASACNVCLDPIIYFPMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358

RESULT 3

US-10-165-844-1
; Sequence 1, Application US/10165844
; Publication No. US20030017539A1
; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Hodge, Martin R.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Weich, Nadine S.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding
; FILE REFERENCE: 35800/248302
; CURRENT APPLICATION NUMBER: US/10/165,844
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 09/088,857
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 09/324,465
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 09/464,685
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/741,783
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/145,745
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: US 09/383,745
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 09/234,923
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: US 09/340,880
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-165-844-1

Query Match 100.0%; Score 1874; DB 12; Length 358;
Best Local Similarity 100.0%; Pred. No. 6,3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNPLTLAKLPNNELHGOESHNSGNRSDGPKNTTLNNEPDTIVLPVYLIIIFVASILLN 60
Db 1 MGNPLTLAKLPNNELHGOESHNSGNRSDGPKNTTLNNEPDTIVLPVYLIIIFVASILLN 60
QY 61 GLAWMIFPHIRNKTSIFLYLKNIVADLIMTLTPPRIVHDAGPGPWYFKFLLCRYSVL 120
Db 61 GLAWMIFPHIRNKTSIFLYLKNIVADLIMTLTPPRIVHDAGPGPWYFKFLLCRYSVL 120
QY 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMTSITFTKVLSCVWVIMAVLSLPIIILT 180
Db 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMTSITFTKVLSCVWVIMAVLSLPIIILT 180
QY 181 NGQPTEDNIDHCSKLSPLGVKMTAVTVVNSCLFVAVVILIGCYIAISRYIHKSROP 240
Db 181 NGQPTEDNIDHCSKLSPLGVKMTAVTVVNSCLFVAVVILIGCYIAISRYIHKSROP 240
QY 241 ISQSRKRKNOSIRVVAVVFTCFPLPYHLCRIPFTSHDRLLDDESAOKILYYCKEITL 300
Db 241 ISQSRKRKNOSIRVVAVVFTCFPLPYHLCRIPFTSHDRLLDDESAOKILYYCKEITL 300
QY 301 FLASACNVCLDPIIYFPMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358
Db 301 FLASACNVCLDPIIYFPMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358

RESULT 4

US-10-225-567A-418
; Sequence 418, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 418
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-418

Query Match 100.0%; Score 1874; DB 14; Length 358;
Best Local Similarity 100.0%; Pred. No. 6,3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGFNLTAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEFDITVLPVLYLIIFVASIILN 60
1 MGFNLTAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEFDITVLPVLYLIIFVASIILN 60
61 GLAWIFPHIRNKTSFIYLNKIIVADLIMLTLPFRIVHDAGFGPMWFKFLCRYSVL 120
61 GLAWIFPHIRNKTSFIYLNKIIVADLIMLTLPFRIVHDAGFGPMWFKFLCRYSVL 120
121 FYANNYSIVFLGLISIDRYLKVKRPFDSRMYSITFTKVLSCVWVMVAVLSLNNIL 180
121 FYANNYSIVFLGLISIDRYLKVKRPFDSRMYSITFTKVLSCVWVMVAVLSLNNIL 180
181 NGOPTEDNIHDCSKLSPGLGKMTAVTYVNSCLFVAVLVILIGCYIASRYIHKSROF 240
181 NGOPTEDNIHDCSKLSPGLGKMTAVTYVNSCLFVAVLVILIGCYIASRYIHKSROF 240
241 ISQSRKKRKNQSIKRVVAVFETCPFLPYHLGRIPFTFSLDRDLDESAOKILYYCKEITL 300
241 ISQSRKKRKNQSIKRVVAVFETCPFLPYHLGRIPFTFSLDRDLDESAOKILYYCKEITL 300
301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSSEVRYYDYTDV 358
301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSSEVRYYDYTDV 358

RESULT 5
US-10-295-027-364
Sequence 364, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Glen, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezl, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 364
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-364

Query Match 100.0%; Score 1874; DB 15; Length 358;
Best Local Similarity 100.0%; Pred. No. 6,3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGFNLTAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEFDITVLPVLYLIIFVASIILN 60
1 MGFNLTAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEFDITVLPVLYLIIFVASIILN 60
61 GLAWIFPHIRNKTSFIYLNKIIVADLIMLTLPFRIVHDAGFGPMWFKFLCRYSVL 120
61 GLAWIFPHIRNKTSFIYLNKIIVADLIMLTLPFRIVHDAGFGPMWFKFLCRYSVL 120
121 FYANNYSIVFLGLISIDRYLKVKRPFDSRMYSITFTKVLSCVWVMVAVLSLNNIL 180
121 FYANNYSIVFLGLISIDRYLKVKRPFDSRMYSITFTKVLSCVWVMVAVLSLNNIL 180
181 NGOPTEDNIHDCSKLSPGLGKMTAVTYVNSCLFVAVLVILIGCYIASRYIHKSROF 240
181 NGOPTEDNIHDCSKLSPGLGKMTAVTYVNSCLFVAVLVILIGCYIASRYIHKSROF 240
241 ISQSRKKRKNQSIKRVVAVFETCPFLPYHLGRIPFTFSLDRDLDESAOKILYYCKEITL 300
241 ISQSRKKRKNQSIKRVVAVFETCPFLPYHLGRIPFTFSLDRDLDESAOKILYYCKEITL 300
301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSSEVRYYDYTDV 358
301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSSEVRYYDYTDV 358

RESULT 6
US-10-295-027-1255
Sequence 1255, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Glen, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezl, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394

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; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1255
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1255

Query Match      100.0%; Score 1874; DB 15; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNLTLAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILIN 60
DB 1 MGNNLTLAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILIN 60
QY 61 GLAWIFPHIRNKTSIFLYLKNIVVADLIMTLTPPRIIVHDAGFGPWYFKFLCRYSVL 120
DB 61 GLAWIFPHIRNKTSIFLYLKNIVVADLIMTLTPPRIIVHDAGFGPWYFKFLCRYSVL 120
QY 121 FYANNMTSIVPLGLISIDRYLKVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
DB 121 FYANNMTSIVPLGLISIDRYLKVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
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DB 181 NGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFPAVALVILIGCYIAISRYIHKSROF 240
QY 241 ISQSSRRKRNQSIIRVVAVPFTCFPLPYHLCRIPTFTSHLDRLDESAQKILYYCKEITL 300
DB 241 ISQSSRRKRNQSIIRVVAVPFTCFPLPYHLCRIPTFTSHLDRLDESAQKILYYCKEITL 300
QY 301 FLSACNVCLDPIIYFFMCRSFRRLLFKKSNIRTRSEIRSLQSVRSEVRYYDYTDV 358
DB 301 FLSACNVCLDPIIYFFMCRSFRRLLFKKSNIRTRSEIRSLQSVRSEVRYYDYTDV 358

RESULT 7
US-10-188-832-135
; Sequence 135, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Nataeha
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer. Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
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; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 135
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-135

Query Match      100.0%; Score 1874; DB 16; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNLTLAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILIN 60
DB 1 MGNNLTLAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILIN 60
QY 61 GLAWIFPHIRNKTSIFLYLKNIVVADLIMTLTPPRIIVHDAGFGPWYFKFLCRYSVL 120
DB 61 GLAWIFPHIRNKTSIFLYLKNIVVADLIMTLTPPRIIVHDAGFGPWYFKFLCRYSVL 120
QY 121 FYANNMTSIVPLGLISIDRYLKVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
DB 121 FYANNMTSIVPLGLISIDRYLKVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
QY 181 NGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFPAVALVILIGCYIAISRYIHKSROF 240
DB 181 NGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFPAVALVILIGCYIAISRYIHKSROF 240
QY 241 ISQSSRRKRNQSIIRVVAVPFTCFPLPYHLCRIPTFTSHLDRLDESAQKILYYCKEITL 300
DB 241 ISQSSRRKRNQSIIRVVAVPFTCFPLPYHLCRIPTFTSHLDRLDESAQKILYYCKEITL 300
QY 301 FLSACNVCLDPIIYFFMCRSFRRLLFKKSNIRTRSEIRSLQSVRSEVRYYDYTDV 358
DB 301 FLSACNVCLDPIIYFFMCRSFRRLLFKKSNIRTRSEIRSLQSVRSEVRYYDYTDV 358

RESULT 8
US-10-692-605-18
; Sequence 18, Application US/10692605
; Publication No. US20040091928A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN
; FILE REFERENCE: 28341/6276 NX1
; CURRENT APPLICATION NUMBER: US/10/692,605
; PRIOR FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US 09/698,419
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 09/481,794
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 09/454,399
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 09/429,517
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,555
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,676
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,695
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/428,114
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/428,020
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/427,859
; PRIOR FILING DATE: 1999-10-27
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Remaining Prior Application data removed - See file Wrapper or PALM.

NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 18
LENGTH: 358

TYPE: PRT
ORGANISM: Homo sapiens
US-10-692-605-18

Query Match 99.6%; Score 1867; DB 16; Length 358;

Best Local Similarity 99.7%; Pred. No. 2.7e-161;

Matches 357; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MGFNLTLLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILLN 60
Db 1 MGFNLTLLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILLN 60

Qy 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTLPFRIVHDAGFGPMWFKFILLCRYSVL 120
Db 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTLPFRIVHDAGFGPMWFKFILLCRYSVL 120

Qy 121 FYANNYSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIILLT 180
Db 121 FYANNYSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIILLT 180

Qy 181 NGOPTEDNIDHCSKSLKSPGLGKMTAVTYNSCLFVAVLVILIGCYIAISRYIHKSROF 240
Db 181 NGOPTEDNIDHCSKSLKSPGLGKMTAVTYNSCLFVAVLVILIGCYIAISRYIHKSROF 240

Qy 241 ISGSRKRKNQSIIRVVAVFTGCLPYHLCRIPFTSHLDRLDESAOKILYYCKEITL 300
Db 241 ISGSRKRKNQSIIRVVAVFTGCLPYHLCRIPFTSHLDRLDESAOKILYYCKEITL 300

Qy 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIIRLSQSVRSSEVRITYDDTV 358
Db 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIIRLSQSVRSSEVRITYDDTV 358

```

RESULT 9

US-09-919-172-22
Sequence 22, Application US/09919172

Patent No. US20020119463A1
GENERAL INFORMATION:

APPLICANT: Fairis, Mary

APPLICANT: Turner, Christopher M.

TITLE OF INVENTION: PROSTATE CANCER MARKERS

FILE REFERENCE: PA-0036 US

CURRENT APPLICATION NUMBER: US/09/919,172

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/222,469

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PERL Program

SEQ ID NO 22

LENGTH: 358

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. US20020119463A1 1650519CD1
US-09-919-172-22

Query Match 98.5%; Score 1846; DB 9; Length 358;

Best Local Similarity 98.6%; Pred. No. 2.2e-159;

Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 MGFNLTLLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILLN 60
Db 1 MGFNLTLLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILLN 60

Qy 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTLPFRIVHDAGFGPMWFKFILLCRYSVL 120
Db 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTLPFRIVHDAGFGPMWFKFILLCRYSVL 120

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Qy 121 FYANNYSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIILLT 180

Db 121 FYANNYSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIILLT 180

Qy 181 NGOPTEDNIDHCSKSLKSPGLGKMTAVTYNSCLFVAVLVILIGCYIAISRYIHKSROF 240

Db 181 NGOPTEDNIDHCSKSLKSPGLGKMTAVTYNSCLFVAVLVILIGCYIAISRYIHKSROF 240

Qy 241 ISGSRKRKNQSIIRVVAVFTGCLPYHLCRIPFTSHLDRLDESAOKILYYCKEITL 300

Db 241 ISGSRKRKNQSIIRVVAVFTGCLPYHLCRIPFTSHLDRLDESAOKILYYCKEITL 300

Qy 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIIRLSQSVRSSEVRITYDDTV 358

Db 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIIRLSQSVRSSEVRITYDDTV 358

RESULT 10

US-09-974-298-86

Sequence 86, Application US/09974298

Patent No. US20020156263A1

GENERAL INFORMATION:

APPLICANT: Chen, Huel-Mei

TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER

FILE REFERENCE: PA-0037 P

CURRENT APPLICATION NUMBER: US/09/974,298

PRIOR FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: 60/238,331

NUMBER OF SEQ ID NOS: 194

SOFTWARE: PERL Program

SEQ ID NO 86

LENGTH: 358

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. US20020156263A1 1650519CD1
US-09-974-298-86

Query Match 98.5%; Score 1846; DB 9; Length 358;

Best Local Similarity 98.6%; Pred. No. 2.2e-159;

Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 MGFNLTLLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILLN 60
Db 1 MGFNLTLLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEPDTIVLPVLYLIIFVASILLN 60

Qy 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTLPFRIVHDAGFGPMWFKFILLCRYSVL 120
Db 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTLPFRIVHDAGFGPMWFKFILLCRYSVL 120

Qy 121 FYANNYSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIILLT 180
Db 121 FYANNYSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIILLT 180

Qy 181 NGOPTEDNIDHCSKSLKSPGLGKMTAVTYNSCLFVAVLVILIGCYIAISRYIHKSROF 240
Db 181 NGOPTEDNIDHCSKSLKSPGLGKMTAVTYNSCLFVAVLVILIGCYIAISRYIHKSROF 240

Qy 241 ISGSRKRKNQSIIRVVAVFTGCLPYHLCRIPFTSHLDRLDESAOKILYYCKEITL 300
Db 241 ISGSRKRKNQSIIRVVAVFTGCLPYHLCRIPFTSHLDRLDESAOKILYYCKEITL 300

Qy 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIIRLSQSVRSSEVRITYDDTV 358
Db 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIIRLSQSVRSSEVRITYDDTV 358

```

RESULT 11

US-10-121-101B-1
Sequence 1, Application US/10121101B

```
Publication No. US20030082653A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti G.
APPLICANT: Jackson, Jennifer L.
APPLICANT: Krasnow, Randi
APPLICANT: Rickett, Paula
TITLE OF INVENTION: GPCR Differentially Expressed in Squamous Cell Carcinoma
FILE REFERENCE: PV-0004 CIP
CURRENT APPLICATION NUMBER: US/10/121,101B
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/470,252
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 08/988,876
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: incyte ID No. US20030082653A1 1650519CD1
US-10-121-101B-1

Query Match
Best Local Similarity 98.5%; Score 1846; DB 14; Length 358;
Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGPNLTATLAKLNNELHGOESHNSGNRSDGPKNTTLHNEPDTVLPLYLIIIPASILLN 60
DB 1 MGPNLTATLAKLNNELHGOESHNSGNRSDGPKNTTLHNEPDTVLPLYLIIIPASILLN 60
QY 61 GLAWMIFPHIRNKTSIFLYLKNIVVADLIMTLFPPRIYHDAGPGWPKFICRYTSL 120
DB 61 GLAWMIFPHIRNKTSIFLYLKNIVVADLIMTLFPPRIYHDAGPGWPKFICRYTSL 120
QY 121 FYANMYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKLSVCWVIMAVLSLNNILT 180
DB 121 FYANMYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKLSVCWVIMAVLSLNNILT 180
QY 121 FYANMYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKLSVCWVIMAVLSLNNILT 180
DB 121 FYANMYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKLSVCWVIMAVLSLNNILT 180
QY 181 NGOPTEDNIDHDSKLSPLGVKMTAVTVVNSCLFVAVLVIIIGCYIAISRYIHKSQOF 240
DB 181 NGOPTEDNIDHDSKLSPLGVKMTAVTVVNSCLFVAVLVIIIGCYIAISRYIHKSQOF 240
QY 241 ISOSRRKRKRNOSIRVVAVVEFTCELPYHLGRIPTFSLDLRLDESQKILYCKEITL 300
DB 241 ISOSRRKRKRNOSIRVVAVVEFTCELPYHLGRIPTFSLDLRLDESQKILYCKEITL 300
QY 241 ISOSRRKRKRNOSIRVVAVVEFTCELPYHLGRIPTFSLDLRLDESQKILYCKEITL 300
DB 241 ISOSRRKRKRNOSIRVVAVVEFTCELPYHLGRIPTFSLDLRLDESQKILYCKEITL 300
QY 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQSVRSEVRIYYDTDV 358
DB 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQSVRSEVRIYYDTDV 358
DB 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQSVRSEVRIYYDTDV 358

RESULT 12
US-10-264-237-2659
Sequence 2659, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA313P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 2659
LENGTH: 196
TYPE: PRT
```

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (160)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (174)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (178)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (177)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (179)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (184)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (186)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (193)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (193)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2659

Query Match
Best Local Similarity 47.4%; Score 889; DB 15; Length 196;
Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGPNLTATLAKLNNELHGOESHNSGNRSDGPKNTTLHNEPDTVLPLYLIIIPASILLN 60
DB 1 MGPNLTATLAKLNNELHGOESHNSGNRSDGPKNTTLHNEPDTVLPLYLIIIPASILLN 60
QY 61 GLAWMIFPHIRNKTSIFLYLKNIVVADLIMTLFPPRIYHDAGPGWPKFICRYTSL 120
DB 61 GLAWMIFPHIRNKTSIFLYLKNIVVADLIMTLFPPRIYHDAGPGWPKFICRYTSL 120
QY 121 FYANMYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKLSVCWVIMAVLSLNNILT 172
DB 121 FYANMYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKLSVCWVIMAVLSLNNILT 172
DB 121 FYANMYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKLSVCWVIMAVLSLNNILT 172

RESULT 13
US-09-919-497-77
Sequence 77, Application US/09919497
Patent No. US2002010662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 77
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-77

Query Match
41.0%; Score 768.5; DB 9; Length 338;
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[illegible]

RESULT 14
 US-09-745-042-13
 / Sequence 13, Application US/09745042
 / Publication No. US20030170777A1
 GENERAL INFORMATION:
 APPLICANT: Conley, Pamela B.
 APPLICANT: Jantzen, Hans-Michael
 APPLICANT: Ramakrishnan-Dubridge, Vanitha
 APPLICANT: Julius, David
 APPLICANT: Hollinger, Gunter
 APPLICANT: COR Therapeutics, Inc.
 TITLE OF INVENTION: F2Y12 Receptor
 FILE REFERENCE: 44481-5053-US
 CURRENT APPLICATION NUMBER: US/09/745, 842
 CURRENT FILING DATE: 2000-12-26
 PRIOR APPLICATION NUMBER: US 60/117, 622
 PRIOR FILING DATE: 1999-12-23
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 13
 / LENGTH: 338
 TYPE: PR1
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: UDP-glucose receptor, KIAA0001 gene product
 US-09-745-042-13

	Query Match	Similarity	41.0%; Score 768.5; DB 10; Length 338;
	Best Local	Similarity	47.6%; Pred. No. 1,6e-61;
	Matches	Conservative	64; Mismatches 97; Indels 1; Gaps 1
Qy	44	VLPVLYLIIIPASILNGLAWIIFPHIRKNSFITYLKIVAVADLMITTPFRPLVHDAG	103
	:	:::	:
Db	24	IIPVLVCWFTAGILNGVSGMIFPVYBSKSFIYLKRIIVADVMSTTFPKLLGSG	83
Qy	104	FGPWFKFKILCRYTSVLEFYANNYSITVEFGILSIDRYLKVNPFGDSRMYSITPFRKLVS	163
	:	:	:
Db	84	LGPQLNVFCRVSALFLPVNNYVSIVFFGLISPRYYKIYKPLMTSFIOSSYSTLSLV	143
Qy	164	CWVIYMAVLSPNILLTNGQPREDIHDCSKSLPGYGVWHAAVYVNSSCLEVAVALVII	223
	:	:::	:
Db	144	IYMMMLMLLAFNILLTNOSVREVTQIKCIELKSELGRKMHAQSNYIFPAIMWIYFLLI	203
Qy	224	GCTAIAISRHYHKS-RQPIQSRSRRKINQSIIRVVAVAFETCFELPYHLCRIPFTESHDR	282
	:	: :	: ::::

Db 204 VFATATATKIKPFKSHKSSNSNSTSVYKCKSSRNIFSVFVFCVCPVYHARIPRYKSTQEA 263

Qy 283 LDEASOKIILYYCKEITLTFPLSACNYCLDPIITLYPFACRSFRRLLPKKSIIRIRRSSTISLQ 342

Db 264 HYSOGCKELTRMRKETLLSLANVCDDPIITLYFCQPFRRILCKLKHIPKAGNDIDIS 323

Qy 343 SVRRSEVRI 351

Db 324 RIRKGNITLL 332

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RESULT 15
US-10-433-146-1
Sequence 1, Application US/10433146
Publication NO. US20040072259A1
GENERAL INFORMATION:
APPLICANT: Scadden, David T.
APPLICANT: Lee, Byoung-Chel
TITLE OF INVENTION: METHODS AND PRODUCTS FOR MANIPULATING
TITLE OF INVENTION: HEMATOPOIETIC STEM CELLS
FILE REFERENCE: M00765.70039. US
CURRENT APPLICATION NUMBER: US/10/433,146
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: PCT/US01/45076
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: U.S. 60/250,727
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 338
TYPES: PRT
ORGANISM: Homo sapiens
US-10-433-146-1

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[illegible]

Search completed: June 1, 2004, 15:20:51
Job time : 49 BECS

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 15:14:35 ; Search time 20 seconds

(without alignments)
1721.828 Million cell updates/sec

Title: US-09-464-685-1

Sequence: 1 MGFLVTLAKLPNNELHGOES.....RSLQSVRSSEVRIYDYTDV 358

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 203366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 203366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	375.5	20.0	342	2	S13638 platelet-activating
2	360	19.2	341	2	S43252 platelet-activating
3	356.5	19.0	341	2	S63666 platelet-activating
4	349	18.6	399	2	I48705 proteinase activat
5	348.5	18.6	365	2	S68679 G protein-coupled
6	346	18.5	397	2	S66518 proteinase-activat
7	345	18.4	342	2	B45680 G protein-coupled
8	340.5	18.2	342	2	A40191 platelet-activatin
9	328	17.5	362	2	S33733 G protein-coupled
10	327	17.4	362	2	I57940 somatostatin recep
11	326	17.4	373	2	JC4162 P2Y receptor - bov
12	325	17.3	373	2	ATP receptor - bov
13	324.5	17.3	373	2	A47556 ATP receptor P2u -
14	324.5	17.3	420	2	I51667 thrombin receptor
15	321.5	17.2	308	2	I50241 G protein-coupled
16	320.5	17.1	352	2	A45747 neuropeptide Y/pep
17	313.5	16.7	352	2	G00048 fusin (leSTRA) - c
18	312.5	16.7	370	2	JC5549 heptahelical p2ys-
19	311.5	16.6	375	2	A54946 P-2U nucleotide re
20	311.5	16.6	400	2	I56553 mu opiate receptor
21	311	16.6	428	2	S30508 probable G protein
22	310.5	16.6	398	2	I56517 mu opioid receptor
23	309.5	16.5	353	2	S28787 neuropeptide Y/pep
24	309.5	16.5	398	2	I56504 mu opioid receptor
25	309.5	16.5	398	2	A57510 mu opioid receptor
26	309	16.5	428	2	A44021 somatostatin recep
27	308	16.4	344	2	T09508 intron 17 purinerg
28	307	16.4	360	2	A57160 chemokine (C-C) re
29	306.5	16.4	363	2	I57955 somatostatin recep

30	306.5	16.4	392	2	S65693 opioid receptor mu
31	306	16.3	364	2	JN0763 somatostatin recep
32	305.5	16.3	418	2	A46226 somatostatin recep
33	305	16.2	380	2	A55259 kappa opioid recep
34	303	16.2	391	2	A39297 somatostatin recep
35	301.5	16.1	35	2	I38435 angiotensin II rec
36	301	16.1	359	2	S15403 angiotensin II rec
37	300.5	16.0	364	2	JQ1488 bradykinin B2 rece
38	300	16.0	391	2	A41795 somatostatin recep
39	300	16.0	391	2	A41795 somatostatin recep
40	298	15.9	356	2	I49340 MIP-1 alpha recept
41	296	15.8	359	2	I39418 angiotensin II rec
42	295.5	15.8	380	2	S36143 kappa opioid recep
43	295	15.7	350	2	A42009 N-formyl peptide r
44	295	15.7	380	2	JC2338 kappa opioid recep
45	294.5	15.7	380	2	A48227 kappa opioid recep

ALIGNMENTS

RESULT 1

S13638 platelet-activating factor receptor - guinea pig

C1Species: Cavia porcellus (guinea pig)

C1Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999

C1Accession: S13638

R1Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To

Nature 349, 342-346, 1991

A1Title: Cloning by functional expression of platelet-activating factor receptor from gu

A1Accession: S13638

A1Status: preliminary

A1Molecule type: mRNA

A1Residues: 1-342 <HON>

A1Cross-references: GB:X56736; NID:949442; PIDN:CAA40060.1; PID:949443

A1Note: The species of guinea pig is not identified, in GenBank entry CCFARREC, release

C1Superfamily: ATP receptor P2u

Query Match 20.0%; Score 375.5; DB 2; Length 342;

Best Local Similarity 27.2%; Pred. No. 6.4e-25;

Matches 96; Conservative 74; Mismatches 148; Indels 35; Gaps 9;

QY	22	NSGNRSDGKNTLNHEDFIVLVLTLFFVSLNGLAVIPIFI---RMTSTPIF 78
DB	4	NSSSRVD-----SEFRYTLFPYVSIIFVLGIANGVAVFAPRLYPSKKLNEIKI 54
QY	79	YLKNIIVVADLIMTLTPPRIYVHADGFGPWYFKFLICRYTSVLPYANMTYSIVPLQLSID 138
DB	55	FMNVLTVADLLFLTLPLMITYYNGQNWFLPKFLCNLAGCLFINTYCSVAFGLVITVN 114
QY	139	RYLVNVPFGDSRMYSITFTKVLSCVAVNA-----VLSLPIIITNCOPTEDNID 191
DB	115	RFQAVKPIKTAQATTRKGIALLSLVIAVAASYFLVMDSTNVV---SNKAGSGNITR 172
QY	192	CSKLKSPFGVKNHATVYVNSCL---FAVAVIILGICIAISRYIHKSRSQFIQSSSR-- 246
DB	173	CFEYVE---KSKRPVLIHICIVLGFYVLLILFCVLV---IHTLLRPVQQRNAE 225
QY	247	-KRRKNSIRVVAVVFETCPFLPYLRCRIPFTFSHLDRLDSSAOKILYYCEITLFLSAC 305
DB	226	VRRALMVCIVLAVFVFCFPHMVOQLPWLALIG--MPPSSNQAIIDADAQVTLCLIST 284
QY	306	NVCLDPIIYFMCSPFSRRLFKKSNITRSEISRLQSVRSSEVRIYDYTDV 358
DB	285	NCVLDPIYVCPITKFKRHLSEKLNIRSSQKCGSRVTTDTGTMAIPINHPIV 337

RESULT 2

S43252 platelet-activating factor receptor - rat
C1Species: Rattus norvegicus (Norway rat)
C1Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999

QY 321 FSR---RLEKSNIRTRRSIRS 340
DB 315 YKKRYMKLRKROVSVSISAVXS 337

RESULT 8

A40191
platelet-activating factor receptor - human
C/Species: Homo sapiens (man)
C/Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #ext_change 20-Jun-2000
C/Accession: A40191; JH0479; A41079; JCI359; A42831; I51923
R/Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A/Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell sur
A/Reference number: A40191; MUID:92250505; PMID:1374385
A/Accession: A40191
A/Molecule type: mRNA
A/Residues: 1-342 <KUN>
A/Cross-references: GB:M6674; NID:9456293; PIDN:AAA60002.1; PID:9456294
R/ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochran, C.G.
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A/Title: Characterization of a human cDNA that encodes a functional receptor for platele
A/Reference number: JH0479; MUID:92028922; PMID:1656963
A/Accession: JH0479
A/Molecule type: mRNA
A/Residues: 1-342 <YER>
A/Cross-references: GB:M80436; NID:9189537; PIDN:AAA60001.1; PID:9189538
A/Experimental source: granulocyte, cell line HL-60 all
R/Nakamura, M.; Honda, Z.; Isumi, T.; Sakana, C.; Mutoh, H.; Minami, M.; Bito, H.; Sey
J. Biol. Chem. 266, 20400-20405, 1991
A/Title: Molecular cloning and expression of platelet-activating factor receptor from hu
A/Reference number: A41079; MUID:92041873; PMID:1657923
A/Accession: A41079
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-342 <NAK>
A/Cross-references: GB:D10202; GB:D90433; NID:9219975; PIDN:BA01050.1; PID:9219976
R/Stumico, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurechi, Y.
Biochem. Biophys. Res. Commun. 189, 617-624, 1992
A/Title: Molecular cloning and characterization of the platelet-activating factor recept
A/Reference number: JCI359; MUID:93112021; PMID:1281995
A/Accession: JCI359
A/Molecule type: mRNA
A/Residues: 1-315, 'N', 317-342 <SUG>
A/Experimental source: heart
A/Note: The authors translated the codon AAT for residue 316 as Lys
R/Seyfied, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.
Genomics 13, 832-834, 1992
A/Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns
A/Reference number: A42831; MUID:92347886; PMID:1322356
A/Accession: A42831
A/Molecule type: DNA
A/Residues: 1-226, 'TG', 229-342 <SEY>
A/Cross-references: GB:M8177; NID:9190697; PIDN:AAA60214.1; PID:9190698
A/Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBI:P:109814)
R/Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993
A/Title: Cloning of a human platelet-activating factor receptor gene: evidence for an in
A/Reference number: I51923; MUID:93192035; PMID:8383507
A/Accession: I51923
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-342 <RES>
A/Cross-references: GB:S56396; NID:9298580; PIDN:AA025755.1; PID:9298581
C/Genetics:
A/Gene: GDB:PTAFR
A/Cross-references: GDB:128806; OMIM:173393
A/Map position: 1p35-1p34.3
C/Superfamily: ATP receptor P2u
C/Keywords: G protein-coupled receptor; transmembrane protein
F:17-38/Domain: transmembrane #status predicted <TR>
F:54-75/Domain: transmembrane #status predicted <TR>

F:92-113/Domain: transmembrane #status predicted <TR>
F:134-155/Domain: transmembrane #status predicted <TR>
F:184-205/Domain: transmembrane #status predicted <TR>
F:233-253/Domain: transmembrane #status predicted <TR>
F:277-297/Domain: transmembrane #status predicted <TR>

Query Match 18.2%; Score 340.5; DB 2; Length 342;
Best Local Similarity 26.7%; Pred. No. 6.8e-22;
Matches 89; Conservative 70; Mismatches 13; Indels 35; Gaps 10;

QY 30 PCKNTTTHNEPDTLVPLVYLIFVASTLGLAVWIF--FHIRKTSIFLYKNIVVA 86
DB 3 PHDSHMSSEPRYLFPVYSIIFVLGANGVLMWAFARLPCKKFEIKI FWNILTPA 62
QY 87 DLMITLPPRPIVDAGSGPWYFKFLICRYTSVLFYANMTYSIFLGISIDRYLKVKVP 146
DB 63 DMLFLITLPLWIVYQNGNMLPKFLCNVAGCLFVITVCSVAFGLVITNFOAVTRP 122
QY 147 F----GDSRMYSIFFTKLVSCVWVIMAVLSLPNIIL--TNGOPT---EDNIHDC---S 193
DB 123 IKTAQANTRKRGIS-----LSVIMVAVGASVFLILDSTVTPDSAGSGVTRCFEHYE 178
QY 194 KLSKPLGVKMTAVTVYNSCLFVAVLVILGCTYAIRSYHKSSRQFISQSRKRNQS 253
DB 179 KGSVPVIL-IHIFIVF-----SFPLVFLITLFCNLIITRLMQPVQOQNAEVRRLM 233
QY 254 IRVVAVFPECFEFLVYLCRIFFPFSHLDRLLDESAOKIYCKEITLPLSACNVCLDPII 313
DB 234 VCTVLAVFITCFVHHVQVLPWTLAEIG-FQDSKPHQAINDAHOVTCLSTNCVLDPIV 292
QY 314 YFMCRSFSPRLPFKSNIRTRSESIRLSQSVR 346
DB 293 YCFILTKFRKRL-----TEKFSMRSSRK 316

RESULT 9

S33733
G protein-coupled receptor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 24-Sep-1999
C/Accession: S33733
R/Webb, T.E.; Simon, J.; Krishak, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock
FEBS Lett. 324, 219-225, 1993
A/Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A/Reference number: S33733; MUID:93285340; PMID:8508924
A/Accession: S33733
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-362 <WEB>
A/Cross-references: EMBL:X73268; NID:9395084; PIDN:CAA51716.1; PID:9395085
C/Superfamily: ATP receptor P2u
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 17.5%; Score 328; DB 2; Length 362;
Best Local Similarity 27.3%; Pred. No. 8.6e-21;
Matches 91; Conservative 62; Mismatches 130; Indels 50; Gaps 12;

QY 40 EDTIVLPVYLIIIVASILNGLAVWIF-FHIRKTSIFLYKNIVVADLIMTLTPPFI 98
DB 38 FQFYFLPLVYLIVLITFELGNSVAIMFVPMRWSGISVYMFNLADPLVYTLPLAI 97
QY 99 VHDAGFGPWYKFTLCRYTSVLFYANMTYSIVFLGISIDRYLKVPFGDSRMYSITFT 158
DB 98 FYFNKTDMLFGDMCKLQRFIFVNLXGSLIFLTCTSVHRYGVVPLKSLGKLKQNA 157
QY 159 KVLSCVWVIMAVLSLPIIITNGQPTEDN---IHDCSLKSLGVKMTAVTVYNS-- 212
DB 158 VYVSLWALVAVVIAV-ILFYSGTGVRRKNTICYDT-----TADERYLSYF 204
QY 213 ----C----LFAVLVLILGCT-IAISRYHKSSRQFISQSRKRNQSVRVVAVFT 263
DB 205 VYSMCTVFECPVIFVILGCTGLIVALKYKD---LDNSPLRKRSIYVITVAVF 260

Qy 264 CFLPYHL-----CRIPFTHSLDRLLDESAQKILYYCKEITLPLASACNVCLDPIIYFF 316
 Db 261 SYLEPHVWKTNLRLARLDFQTPQMCAPNDK-----VATYQVTRGLASLNSGVDPILYFL 315
 Qy 317 MCRSFSRRLFKKSNIRTSSESIRLSQSVR-RSE 348
 Db 316 AGDFRRRLSR-----ATRKSSRSRSEPNVQSKSE 344

RESULT 10

157940

somatostatin receptor 5 - rat

N:Alternate names: somatostatin release-inhibiting factor subtype 28 receptor

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 24-Nov-1999

C:Accession: 157940; 157949; S39244

R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.

Mol. Pharmacol. 44, 939-946, 1992

A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pred

A:Reference number: 157940; MUID:93125499; PMID:1362243

A:Accession: 157940

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-363 <OCA1>

A:Cross-references: GB:I04535; NID:G409238; PIDN:AAA17029.1; PID:G409239

R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.

Mol. Pharmacol. 44, 1278, 1993

A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pred

A:Reference number: 157949; MUID:94088493; PMID:8264565

A:Accession: 157949

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 341-363 <OCA2>

A:Cross-references: GB:S57370; NID:G455947; PIDN:AA29371.1; PID:G455948

A:Experimental source: pituitary

R:Penetta, R.; Greenwood, M.; Patel, Y.C.

submitted to the EMBL Data Library, August 1993

A:Description: Correction of the nucleotide and amino acid sequence of the rat somatost

A:Reference number: S39244

A:Accession: S39244

A:Molecule type: mRNA

A:Residues: 309-363 <PEN>

A:Cross-references: EMBL:X74828; NID:G433911; PIDN:CAA52825.1; PID:G433912

C:Genetics:

A:Gene: SSTR5

C:Superfamily: vertebrate rhodopsin

Query Match 17.4%; Score 327; DB 2; Length 363;

Best Local Similarity 29.3%; Pred. No. 1.1e-20;

Matches 99; Conservative 62; Mismatches 139; Indels 38; Gaps 14;

Qy 5 LTLAKLNNELHGOESHSNGRSDGPKNTLLHNEFD-----TIVLPVLYIILFVASTLL 59
 Db 4 LSLASTP-----SNASAAASG-SNNWSLVGSASPMGARAVLVLPVLYLIVCTVGS 54
 Qy 60 NGLAWIIF-HIRNKTSIFLYKNIIVVADLMTLTFPRRIYHDAFGWYKFLICRTS 118
 Db 55 NTLVIVVLRHAKMTVTNNVILNLAVDVLFMLDPLFATONAAVSVWPGSFLCRLVM 114
 Qy 119 VLFYANWTSIVFLGLSIDRYLKVKKPGDSRMYSITFTKVLSCVWVIMAVSLPNI 178
 Db 115 TLIDGNGTSTIFCLMVMVDRLAVVHPLRSARMRPRVAVASAAVAVFSLMSLPLV 174
 Qy 179 LTNQGFEDNIDGS-KLKSPGLVKMHTA-VTVNSCLFVAVLVILICYIAISRYHKS 236
 Db 175 PAD--VQEGWGTCLNSWPEPVGL-WGAAPITYTSLVLFPGFLVICCYLLIVKV-KA 229
 Qy 237 SRQFISQSRK--KHQSIKRVVAVAFETCLP--HICRIPTFSLHRLDLSAQK 290
 Db 230 AGMRGSSRRRRSEPKVRMVVVVAVLVGVGCLPFIIVINVLAF-----LPEEPTSA 283
 Qy 291 ILYYCKEITLPLASACNVCLDPIIYFFMCRSFSRRLFKK 328

Db 284 GLYF---FVVVLSYANSCANPLLYGLPSDNF-RQSFRR 317

RESULT 11

JC4162

p2y receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 12-Oct-1995 #sequence revision 10-Nov-1995 #text_change 24-Sep-1999

C:Accession: JC4162

R:Henderson, D.J.; Elliott, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.

Biochem. Biophys. Res. Commun. 212, 648-656, 1995

A:Title: Cloning and characterisation of a bovine p2y receptor.

A:Reference number: JC4162; MUID:95352058; PMID:7626079

A:Accession: JC4162

A:Molecule type: mRNA

A:Residues: 1-373 <HEN>

A:Cross-references: EMBL:X87628; NID:G1032484; PIDN:CAA60958.1; PID:G1032485

A:Experimental source: aortic endothelial cell

C:Genetics:

A:Gene: bopy2y

C:Superfamily: ATP receptor P2u

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:52-77/Domain: transmembrane #status predicted <TM1>

F:88-111/Domain: transmembrane #status predicted <TM2>

F:124-150/Domain: transmembrane #status predicted <TM3>

F:171-191/Domain: transmembrane #status predicted <TM4>

F:214-237/Domain: transmembrane #status predicted <TM5>

F:261-282/Domain: transmembrane #status predicted <TM6>

F:305-328/Domain: transmembrane #status predicted <TM7>

F:11,27,113,197/Binding site: carbohydrate (asn) (covalent) #status predicted

F:258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 17.4%; Score 326; DB 2; Length 373;

Best Local Similarity 25.6%; Pred. No. 1.3e-20;

Matches 87; Conservative 69; Mismatches 132; Indels 52; Gaps 9;

Qy 30 PGKNTLLHNEFDITVLPVLYIIFVASTLLGLAWIF-FHIRNKTSIFLYKNIIVADL 88
 Db 39 PFKALTKTGQFYLPLAVIILVFLITGLNSVAIMFVFMKPRSGISVYMFNLADF 98
 Qy 89 IMTLFPRRIYHDAFGWYKFLICRTSVLFYANWTSIVFLGLSIDRYLKVKKPG 148
 Db 99 LVLVTLPLIIFYFNKTDWIRGDMCKLGRIFHNVLCGILFICSAHRYSGVVPYLK 158
 Qy 149 DSRKYSITFTKVLSCVWVIMAVSLPNIITNQPEDNIDHDSKLSPLGKMTAVT 208
 Db 159 SLGRLLKKNNAVYISLVWLIV-VGISPILFVSG-----TGIRNKRTIT 201
 Qy 209 -----YVNS-----CLFVAVLVILICGY-IAISRYTHKSRQFISQSRK 249
 Db 202 CYDTTSDBELSYIYKMTVMNFVPLVILICGYIGLIVALLYKD---LNSPLRK 257
 Qy 250 HNSIRVVAVAFETCLPFLYLCRIPTFSLHRLDLS--SAQKILYYCKEITLPLASCNV 307
 Db 258 SIYVIVIVLVFAVSYIPFHWKMTMNLRLARLDFQTPQMCAPNDRVATYQVTRGLASLNS 317
 Qy 308 CLDPIIYFFMCRSFSRRLFK-----KSNITRSTSI 338
 Db 318 CVDPILVFLAGDFRRRLSRATRKASRSRSEANLQSKSDM 357

RESULT 12

JC4737

G protein-coupled receptor P2Y1 - human

N:Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C:Species: Homo sapiens (man)

C>Date: 10-May-1996 #sequence revision 16-Aug-1996 #text_change 17-Nov-2000

C:Accession: JC4737; S54253

R:Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.

Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A:Title: Cloning and tissue distribution of the human P2Y1 receptor.

A:Reference number: JC4737; MUID:96205320; PMID:8630005

A:Accession: JC4737

Db 210 LSWRTMSRAYMASCPIWMLISASTIPILVTEBOTQKIPRLDITTCCHVDLKDQ---LKDQY 266
QY 206 AVTYVNSCL--FVAVLVLLIGCYTASIRYIKSSQPIISQSRKRNQSIKRVVAVVFT 263
Db 267 IYFSSSFLFFVFPFIIITTCYIGIIRSLSSS---IENSCKTRALFLAVVLCVPII 323
QY 264 CFLPYHLGRIPFTFSLRLDLSAOKILYYCKEITLFLSACNVCGLDPIIYFPMCRSPSR 323
Db 324 CFGP---TNVLPITYL-----QEANRFLYFAYILSACVSVSCCLDPIIYYVASQQR 375
QY 324 RLFKKSNIRTRSE 336
Db 376 YLYSLCCRKVSE 388

RESULT 15

150241
G protein-coupled receptor 6H1 - chicken
N:Alternate names: purinoceptor 6H1
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000
C:Accession: 150241; J04618
R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J:Immunol. 151, 628-636, 1993
A>Title: Identification of a G protein coupled receptor induced in activated T cells.
A:Reference number: 150241; MUID:93329058; PMID:8393036
A:Accession: 150241
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-308 <KAP>
A:Molecule type: mRNA
A:Cross-references: GB:L06109; NID:G304383; PIDN:AB06587.1; PID:G304384
R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A>Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A:Reference number: J04618; MUID:96190677; PMID:8619790
A:Accession: J04618
A:Molecule type: mRNA
A:Residues: 1-308 <WEB>
A:Cross-references: GB:L06109; NID:G304383; PIDN:AB06587.1; PID:G304384
A:Experimental source: T-cells
C:Comment: This receptor plays a role in T-cell activation.
C:Gene: P2Y5
A:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein
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F:51-74/Domain: transmembrane #status predicted <TM2>
F:89-109/Domain: transmembrane #status predicted <TM3>
F:133-153/Domain: transmembrane #status predicted <TM4>
F:177-201/Domain: transmembrane #status predicted <TM5>
F:227-248/Domain: transmembrane #status predicted <TM6>
F:269-292/Domain: transmembrane #status predicted <TM7>

Query Match 17.2% Score 321.5; DB 2; Length 308;
Best Local Similarity 27.7% Pred. No. 2.7e-20;
Matches 86; Conservative 67; Mismatches 135; Indels 23; Gaps 9;

QY 33 NTLTNEEDTIVLPVLYLIIFVASILNGLAVWIF--FHIRNKTSFIYLNIVADLI 89
Db 5 NCSTEDSFYTLVYGCVFSNVFLGLIANCAIYIFTLKVRNETT--TYMLNLAISDLL 62
QY 90 MTLTFPPRIVMDAGCPWFYKFIILCRYTSVLFYANMTSIVFLGLISIDRYLKAVKPFQD 149
Db 63 FVFTLPFRIVYFV-VRNMPFGDVLCKISVTLFYTMYGSLPLTLCISVDRFLAIVHFRS 121
QY 150 SRMYSITFTKVLSCVWVMAVLSLPIITL--TNGOPTEDNIDCSKLSPLGVKMH-- 205
Db 122 KTLRKRRARIYCAVMITVLAGSTPASFGSTNRQ---NNTGQRTCPENPPESTMKTYL 178
QY 206 --AVTYVNSCLFVAVLVILIGCYTASIRYIKS---SRQFISQSRKRNQSIKRVVAV 260
Db 179 SRIVIFIEIVGFPIILNVTCSTWVLRNLKPLTLNRKLS----KKVLMIFVHLVI 234

QY 261 FFCFLPYHLGRIPFTFSLRLDLSAOKILYYCKEITLFLSACNVCGLDPIIYFPMCRS 320
Db 235 FCFEFVYNTLILYSIMRQGTWINGSVVAVRMTYPTLCIAVSNCCFDBIYYFTSDT 294
QY 321 FSRRLFKKSNIR 331
Db 295 NS-ELDKKQGV 304

Search completed: June 1, 2004, 15:19:15
Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2004, 15:13:50 ; Search time 45 Seconds
(without alignments)
2510.123 Million cell updates/sec

Title: US-09-464-685-1
 Perfect score: 1874
 Sequence: 1 MGFNLTLAKLPNNELHQGES.....RSLQSVRRSEVRITYDYTDV 358

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 10170411

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

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1:  sp. archaea:*
2:  sp. bacteri:*
3:  sp. fungi:*
4:  sp. human:*
5:  sp. invertebrate:*
6:  sp. mammal:*
7:  sp. mhc:*
8:  sp. organelle:*
9:  sp. phage:*
10: sp. plant:*
11: sp. rodent:*
12: sp. virus:*
13: sp. vertebrate:*
14: sp. unclassified:*
15: sp. virus:*
16: sp. bacteriap:*
17: sp. archaeap:*

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SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	768.5	41.0	338	4		Q81YT7	Q81Y7 homo sapien
2	692	36.9	347	11		Q8BZV8	Q8BZV8 mus musculus
3	683.5	36.5	342	6		Q8HXH1	Q8HXH1 macaca fasc
4	423	22.6	319	11		Q8CFI3	Q8CFI3 mus musculus
5	422	22.5	319	11		Q8B5S5	Q8B5S5 mus musculus
6	419.5	22.4	319	4		Q81V06	Q81V06 homo sapien
7	419	22.4	319	11		Q8BY85	Q8BY85 mus musculus
8	417	22.3	317	11		Q8BTN1	Q8BTN1 mus musculus
9	381.5	20.4	309	11		Q8K528	Q8K528 mus musculus
10	374	20.0	374	13		O5Y466	O5Y466 meleagris g
11	369	19.7	375	11		Q8BYI1	Q8BYI1 mus musculus
12	369	19.7	376	4		Q7Z3W3	Q7Z3W3 homo sapien
13	368.5	19.7	347	13		Q7ZZA4	Q7ZZA4 brachydactylid
14	355	18.9	339	4		Q8N5S7	Q8N5S7 homo sapien
15	352	18.8	537	13		Q7ZKQ7	Q7ZKQ7 xenopus lae
16	351.5	18.8	358	13		Q7ZXJ7	Q7ZXJ7 xenopus lae

17	350.5	18.7	357	1.1	Q7MW7	Q7MW7 mus musculus
18	350.5	18.7	358	1.3	Q9YCC3	Q9YCC3 xenopus lae
19	348	18.6	359	1.1	Q8R311	Q8R311 mus musculus
20	347.5	18.5	341	1.1	Q8C017	Q8C017 mus musculus
21	347	18.5	353	1.3	Q93C47	Q93C47 cyprinus ca
22	346	18.5	357	1.3	Q9DE05	Q9DE05 raja erinac
23	339	18.1	352	6	Q9TY5	Q9TY5 boe laurus
24	334.5	17.8	354	1.3	Q7ZWY0	Q7ZWY0 xenopus lae
25	334	17.8	337	4	Q81V19	Q81V19 homo sapien
26	332	17.7	342	6	Q9GK76	Q9GK76 capra hircu
27	332	17.7	353	1.3	Q9PF77	Q9PF77 brachydanio
28	330.5	17.6	358	1.3	Q9DD11	Q9DD11 gallus galli
29	330.5	17.6	359	1.1	Q8B3B7	Q8B3B7 mus musculus
30	329.5	17.6	361	1.1	Q8VHP3	Q8VHP3 cavia porce
31	328.5	17.4	176	4	Q8BY11	Q8BY11 homo sapien
32	326.5	17.4	390	1.3	Q8QC04	Q8QC04 carassius a
33	325.5	17.3	352	6	Q7YS92	Q7YS92 tupia bela
34	324	17.4	349	1.1	Q8VD47	Q8VD47 rattus norv
35	324	17.3	359	1.3	Q9PY77	Q9PY77 anguilla an
36	323.5	17.3	342	6	Q9XSD4	Q9XSD4 sus scrofa
37	323.5	17.3	347	6	Q9MZM9	Q9MZM9 ateleas pani
38	323.5	17.3	358	1.3	Q9PUA0	Q9PUA0 acipenser r
39	322.5	17.2	334	6	Q9N130	Q9N130 salmifir bol
40	322.5	17.2	347	6	Q9MZM7	Q9MZM7 callimico g
41	322	17.2	293	1.1	Q8EMJ5	Q8EMJ5 mus musculi
42	321	17.1	296	6	Q9TYV6	Q9TYV6 canis famli
43	320.5	17.1	334	6	Q9N1D3	Q9N1D3 hylobates c
44	320.5	17.1	347	6	Q9MZM6	Q9MZM6 hylobates c
45	320.5	17.1	347	6	Q9MZM5	Q9MZM5 hylobates h

ALIGNMENTS

ID	Q81YV7		PRELIMINARY;	PRT;	338 AA.
AC	Q81YV7				
DT	01-MAR-2003	(TREMBLrel. 23,	Created)		
DT	01-MAR-2003	(TREMBLrel. 23,	Last sequence update)		
DE	01-OCT-2003	(TREMBLrel. 25,	Last annotation update)		
DE	G protein-coupled receptor	105.			
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISUE=Testis;				
RA	Stratberg R.;				
RL	Submitted (JUL-2002) to the EMBL/genbank/DDBJ databases.				
EA	EMBL; BC034989; AAH34989.1; -				
DR	GO: GO:0016021; C:integral to membrane; IEA.				
DR	GO: GO:0004872; F:receptor activity; IEA.				
DR	GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.				
DR	GO: GO:0007186; P:G-protein coupled receptor protein signaln. . . ; IEA.				
DR	InterPro; IPR005276; GPCR_rhodpsn.				
DR	InterPro; IPR005466; UDPG_receptor.				
DR	Pfam; PF00001; Tcm_1; 1.				
DR	PRINTS; PR00237; GPCRRHODPSN.				
DR	PRINTS; PR01655; UDPEUCOSER.				
DR	PROSITE; PS50262; G_PROTEIN_RECCEP_F1_2; 1.				
KW	Receptor.				
SQ	SEQUENCE	338 AA;	38972 MW;	8871408E2F392DDB	CRC64;
Query Match		41.0%;	Score 768.5;	DB 4;	Length 338;
Best Local Similarity		47.6%;	Pred. No. 1,1e-58;		
Matches 147;	Conservative	64;	Mismatches 97;	Indels 1;	Gaps 1

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QY 104 GFWYFKEILCRVTSVLFYANMTSYVFLGISIDRLKVKVPGDSRMYSITFTYLSV 163
DB 84 LGFQGLAVFCVRSVAFLFYANMTSYVFLGISIDRLKVKVPLUMTSFISQSVISKLVS 143
QY 164 CWTYMAVLSLPIIILNGOPTEDNIDCSKSLPGVKMTAVTYVNSCLFVAVALVILI 223
DB 144 IVMMLKMLLAVPNIILTNQSVREVTQKCTELSKELGRKWKASNIYFVAIFMIVFLLI 203
QY 224 GCYIAISRYIHKS-RQFISQSRKRKNSIRVVAVFETCPLPHLCIPTFPHLDR 282
DB 204 VFTAITKKIKFKSLKSSRNSTSVKSSNIFSVFVFCVPHIARIPTKSOQTA 263
QY 283 LDESACKILYCKEITLFLSACVCLDPIIYFMCFSFGRRLFKSNIRTSRSISRLQ 342
DB 264 HYSQSKELIRYKMEFTLLSANVCCLDPIIYFLOQPFREILCKLHPIKQNDLDS 323
QY 343 SVRSSEVRI 351
DB 324 RIRKNTTL 332

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RESULT 2

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Q8BZV8 PRELIMINARY; PRT; 347 AA.
AC Q8BZV8;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE P2Y12 platelet ADP receptor homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SOURCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK034448; BAC28294.1; -.
DR MGD; MGI:1918089; P2Y12.
DR GO; GO:0005887; C:integral to plasma membrane; IEA.
DR GO; GO:0001609; F:adenosine receptor activity; G-protein coupled; IMP.
DR GO; GO:0001621; F:platelet ADP receptor activity; IMP.
DR GO; GO:0007186; P:G-protein signaling; coupled to camp nucleo. . .; IMP.
DR GO; GO:0030168; P:platelet activation; IMP.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01569; P2Y12PRNCPTR.
DR PROSITE; PS50262; G_PROTEIN_RECPT_P1_2; 1.
SQ SEQUENCE 347 AA; 39430 MW; F114688377FE25F1 CRC64;

```

Query Match 36.9%; Score 692; DB 11; Length 347;

Best Local Similarity 43.3%; Pred. No. 4,9e-52;

Matches 136; Conservative 60; Mismatches 102; Indels 16; Gaps 2;

```

QY 28 DQGNKNTTLN-----EPDITVLPVLYLIIFVASILNGLAWIIFHIRN 72
DB 2 DVGWNTTSANTTSPGTSLTCVRDYKITQVLPFLTYVLPFAGLITSLAMRIFFQIRS 61
QY 73 KTSFELYKNIVVALIMTLFPPRIYVDAGGPGVFFELICRTYSVLFYANMTSYVFL 132
DB 62 KSNFIIFKNIVISLMLITLFPFKILSDAKLGAGPLTTLCOVTSVTFYTWYISISFL 121
QY 133 GLISIDRLKVKVPGDSRMYSITFTYLSVLCVWYIMAVLSLPIIILNGOPTEDNIDHC 192
DB 122 GLITIDRLKTKTRPFKISSPSNLGAKILSVIVAFMFLISLPMILNRPKDKDYTKC 181

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QY 193 SLKSLPGVKMTAVTYVNSCLFVAVALVILGCIYIAISRYIHKS-SRQFISQSRKRKN 251
DB 182 SFLKSEFGLVWHEIYVNYICQVLFWINFLIVYCSLITKEHYLSYVTRGSAKVPKKVN 241
QY 252 QSRIVVAVFELCFPYHLICRPFPSHLDLDESACKIYCKEITLFLSACVCLDP 311
DB 242 VQVFTIILAFPLCFVPHIARIPTKSOQTA 301
QY 312 IYFMCFSFGRRL 325
DB 302 FIYFPLCKSFNSSL 315

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RESULT 3

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Q8HXH1 PRELIMINARY; PRT; 342 AA.
AC Q8HXH1;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxId=95411;
RN [1]
RP SOURCE FROM N.A.
RC TISSUE=Medulla oblongata;
RA Hashimoto K., Osada N., Hida M., Kuwada J., Sugano S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RX MEDLINE=21458551; PubMed=11574149;
RA Osada N., Hida M., Kuwada J., Tanuma R., Iseki K., Hirata M., Suto Y.,
RA Hirai M., Terao K., Sunkai Y., Sugano S., Hashimoto K.;
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
RT chromosome."
RL Gene 275:31-37 (2001).
DR EMBL; AB097554; BAC41779.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01569; P2Y12PRNCPTR.
DR PROSITE; PS50262; G_PROTEIN_RECPT_P1_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 342 AA; 39479 MW; 0869FDD014A56FC CRC64;

```

Query Match 36.5%; Score 683.5; DB 6; Length 342;

Best Local Similarity 41.6%; Pred. No. 2,6e-51;

Matches 137; Conservative 69; Mismatches 114; Indels 9; Gaps 5;

```

QY 25 NRSDDGKNTTL--HNEPDTVLPVLYLIIFVASILNGLAWIIFHIRNKTSTFYK 81
DB 6 NLTSABG-NTSLCTRDYKITQVLPFLTYVLPFVGLITSLAMRIFFQIRSKSNFIPLK 64
QY 82 NIYVALDLMITLFPFRIYVDAGGPGVFFELICRTYSVLFYANMTSYVFLGISIDRL 141
DB 65 NIYISDLMLITLFPFKILSDAKLGAGPLTTLCOVTSVTFYTWYISISFLGITIDRYQ 124
QY 142 KVKVPGDSRMYSITFTYLSVLCVWYIMAVLSLPIIILNGOPTEDNIDCSKSLPGV 201
DB 125 KTRPFPKTSNPKNLGLFTKILSVLIMAFMFLISLPMILNRRPRDQNVKCSFLSKSEPL 184
QY 202 KMTAVTYVNSCLFVAVALVILGCIYIAISRYIHKS-SRQFISQSRKRKNQSRIVVA 259

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Db 185 VMEIIVNYICQVLSWINEFLIVCYTLITKEIYRSYVTRGVGKVRK-KYVAVKFIITA 243
 Qy 260 VFPCFCLPYHLCRIPFTSHDLDESAOKILYYCKEITLPLSCANCIDPIIYFPCGR 319
 Db 244 VFPCFVPHARIPYTLISQTRDVPDCAENTLIFYVCKSTLMLSLACIDPIYFLCK 303
 Qy 320 SFSRRLFKKSNIRTSISIRLSQVRSE 348
 Db 304 SFRNSLI--SMLKCPNSATSSQDNKKE 330

RESULT 4

08CIF3 PRELIMINARY; PRT; 319 AA.
 ID 08CIF3
 AC 08CIF3
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Similar to platelet activating receptor homolog.
 GN F730001G15RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RA Strauberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC024054; AAH24054.1; -
 DR MGD; MGI:2442043; F730001G15RIK.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 319 AA; 36705 MW; 11E0D6556B694361 CRC64;

Query Match 22.6%; Score 423; DB 11; Length 319;
 Best Local Similarity 30.9%; Pred. No. 1e-28; Indels 16; Gaps 5;
 Matches 93; Conservative 63; Mismatches 129;

Qy 49 YLIIFVASILNGLAVWIFPH-IRNKTSPFYLNKIIVADLIMLTFFPRIVHDAGFGPW 107
 Db 21 FYLVFLIGIISCFATWAFIOKTNHRCVSYILNLTADPLTLALPVKIIVDIGVAPW 80
 Qy 108 YFKFLCRYTSVLFANNMTSIVPLGLSIDRYLKVKVPGDSRMYSITFTKVLSCVAV 167
 Db 81 KLRIFHCQVTAACLIYNNMYSIIPLAFVISIDRCQLHSCIKYRQEGFAMISAIVWL 140
 Qy 168 IMAVLSLENIITLNGOPTEDNIHDSKSLKSPGVKMTAVTVYNSCLFVAV-LVILIGCY 226
 Db 141 MVLLIMVNMVYIPIKDIKESNVGMEPKKEGFRMHLTNTFCVAIFLNSVILLISNF 200
 Qy 227 IAIISR-YIHKSROFISQSSRRKKNOSIRVVAVFTFCPLPYHLCRIPFTSHDLRLD 285
 Db 201 LAIRQLYNNRNTNTPSVKSL-----LHLLVLTASYIICFVYHNAVRIPYTLISQTEVSD 256
 Qy 286 ESAOKILYYCKEITLFLSACVCLDPIIYFPCGRSF-----SRRLFKKSNIRTSSE 336
 Db 257 CSTRIALPKAKEATLLAVSNLCFDPILYYHLSKAFRLKVTETPASPCKSKPLEERLRS 316
 Qy 337 S 337
 Db 317 N 317

RESULT 5

Q8BG55 PRELIMINARY; PRT; 319 AA.

ID Q8BG55
 AC Q8BG55
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Probable G protein-coupled receptor H963 homolog.
 GN F730001G15RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs".
 RL Nature 420:563-573(2002).
 DR EMBL; AK041381; BAC10925.1; -
 DR EMBL; AK089287; BAC40829.1; -
 DR MGD; MGI:2442043; F730001G15RIK.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1_2; 1.
 SQ SEQUENCE 319 AA; 36719 MW; C2E0D558FB694364 CRC64;

Query Match 22.5%; Score 422; DB 11; Length 319;
 Best Local Similarity 30.6%; Pred. No. 1.3e-28;
 Matches 92; Conservative 64; Mismatches 129; Indels 16; Gaps 5;

Qy 49 YLIIFVASILNGLAVWIFPH-IRNKTSPFYLNKIIVADLIMLTFFPRIVHDAGFGPW 107
 Db 21 FYLVFLIGIISCFATWAFIOKTNHRCVSYILNLTADPLTLALPVKIIVDIGVAPW 80
 Qy 108 YFKFLCRYTSVLFANNMTSIVPLGLSIDRYLKVKVPGDSRMYSITFTKVLSCVAV 167
 Db 81 KLRIFHCQVTAACLIYNNMYSIIPLAFVISIDRCQLHSCIKYRQEGFAMISAIVWL 140
 Qy 168 IMAVLSLENIITLNGOPTEDNIHDSKSLKSPGVKMTAVTVYNSCLFVAV-LVILIGCY 226
 Db 141 MVLLIMVNMVYIPIKDIKESNVGMEPKKEGFRMHLTNTFCVAIFLNSVILLISNF 200
 Qy 227 IAIISR-YIHKSROFISQSSRRKKNOSIRVVAVFTFCPLPYHLCRIPFTSHDLRLD 285
 Db 201 LAIRQLYNNRNTNTPSVKSL-----LHLLVLTASYIICFVYHNAVRIPYTLISQTEVSD 256
 Qy 286 ESAOKILYYCKEITLFLSACVCLDPIIYFPCGRSF-----SRRLFKKSNIRTSSE 336
 Db 257 CSTRIALPKAKEATLLAVSNLCFDPILYYHLSKAFRLKVTETPASPCKSKPLEERLRS 316
 Qy 337 S 337
 Db 317 N 317

RESULT 6

Q8IV06 PRELIMINARY; PRT; 319 AA.
 ID Q8IV06
 AC Q8IV06
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Platelet activating receptor homolog.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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Oy 49 YLIFVAILNGLAWVIFPHIRNKTSFLPYLKNIVADLIMTLTPPRIYHDAGFGWY 108
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 FYLVFLIGITIGSCPTMA-FKTTNRCVSYIYNLTDEFLITLAPKTIIDLVGAHWK 79
Oy 109 FKFLICRYTVLFPYANMTYSIVFLGLISIDRYLKVYKPGDSRWYSITFKYLSVCWVI 168
Db 80 LRFHCQVLAELIYNMTLSITIFLAFVSDIRCLQIHSCIKYRIQEPGAKMISAVWM 139
Oy 169 MAVLSPLIILNGPTEDNIDHCKLSPGKVKHTAVTVNSCLFPAV-LVILIGCI 227
Db 140 VLLIWPVMAIPIDIKERSNVGCFKPEFGRNHLLTNFICVAFILNFSVILISNPL 199
Oy 228 AISR-YHKSRQFISQSRKKNQSIKRVVAVPFTGCELPYHLCRIPFTSHLDRLDE 286
Db 200 AIRQIYRNRDNTNYSVKSAL----LHLLVYASITICFVPHAVRIPITLSQTEVISDC 255
Oy 287 SAOKILYVCKEITLPLSACNVCLDPIYFMCRSF-----SRLLFKSNIRTRSES 337
Db 256 STRIALPFAKEATLLAVSNLCFDPILYVHLSKAFRLKVTETPAAPKSKPLEERLSEN 315

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RESULT 9

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Oy 08R528 PRELIMINARY; PRT; 309 AA.
AC 08R528;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
Db CysLeu1n1 leukotriene 2 receptor.
GN CysLeuR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishii S.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL; AB058930; BAB86881.1; -.
DB MGI; MGI:1917336; CysLeuR2.
DB GO; GO:0001631; F:cycloleuk1 leukotriene receptor activity; IDA.
DB InterPro; IPR004071; CysLeuk receptor.
DB InterPro; IPR000276; GPCR_Rhodopsn.
DB Pfam; PF00001; 7tm_1; 1.
DB PRINTS; PRO1533; CysLTRRECPTR.
DB PRINTS; PRO0237; GPCR_RHODOPSIN.
DB PROSITE; PS50262; G_PROTEIN_RECPEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 309 AA; 35226 MW; 96FACC6B8AF96974 CRC64;

```

Query Match 20.4%; Score 381.5; DB 11; Length 309;
 Best Local Similarity 31.5%; Pred. No. 4e-25;
 Matches 102; Conservative 56; Mismatches 133; Indels 33; Gaps 12;

```

Oy 23 SGNRDGGCKNTLNEEDTIVLPVLYLIIFVASILNGLAWVIFP-HIRNKTSIFLYK 81
Db 4 TGPSSYSNRCTTN-FKREFFYPIIYLIIFWGAINGGFSIYVFLQTCCKSTSVNFWL 62
Oy 82 NIVVADLIMTLTPPRIYHDAGFGWYKFLICRYTVLFPYANMTYSIVFLGLISIDRYL 141
Db 63 NLATSDPLFISTLPRADYIFRGSNMIFGDLACRWMSISLYNMWTSITFLVLSVAF 122
Oy 142 KVVKPGDSRWYSITFK--VLSVCWVIMAVLSLPIIILNGPTEDNIDHC-----S 193
Db 123 ATVHPF--RMFHTVSVSAMILGIIWVF--IMASSALLVNGGEBEKNIISCLELSPQ 177
Oy 194 KLSPLGVKMTAVYVNSCLFPAVAVLILIGCIYASIRYIHKSRQFISQSRKKNQ 253
Db 178 KFKSL-LIMNHAV----AVGFLPLPFLITTCYLLIRLLAB--IPESGPRAHKRA 229
Oy 254 IRVVV---AVFPTCLPYHLCRIPFTSHLDRLDESAOKILYVCKEITLPLSACNVCLD 310

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Db 230 LTTIYAMITFLCFLPYHALRT----LHLVTDKDSGDVHLKATVITLTMAANSQFN 285
Oy 311 PIYFPMCRSFRRL---FKSNI 331
Db 286 PFLYFAGENKARLALFSLVHL 309

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RESULT 10

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Oy 057466 PRELIMINARY; PRT; 374 AA.
AC 057466;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
Db G protein coupled p2y nucleotide receptor.
GN TP2Y.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Blood;
RC MEDLINE=98086419; PubMed=9415702;
RX Boyer J.L., Waldo G.L., Harden T.K.;
RT "Molecular cloning and expression of an avian G protein-coupled p2y
RT receptor.";
RL Mol. Pharmacol. 52:928-934(1997).
DR EMBL; AF031897; AAC60339.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DB InterPro; IPR00276; GPCR_Rhodopsn.
DB Pfam; PF00001; 7tm_1; 1.
DB PRINTS; PRO0237; GPCR_RHODOPSIN.
DB PROSITE; PS00237; G_PROTEIN_RECPEP_FL_1; 1.
DB PROSITE; PS50262; G_PROTEIN_RECPEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 374 AA; 42594 MW; 849C465722BD02B CRC64;

```

Query Match 20.0%; Score 374; DB 13; Length 374;
 Best Local Similarity 29.3%; Pred. No. 2.2e-24;
 Matches 95; Conservative 67; Mismatches 132; Indels 30; Gaps 9;

```

Oy 31 GKNTT-----LHNEFDIVLPVLYLIIFVASILNGLAWVIFP-HIRNKTSIFLYK 81
Db 22 GGNTPAAAEAKCVNEBFKFLIPISYGVFVGLPLSNMAMWIFVSRMRPNVATTVWF 81
Oy 82 NIVVADLIMTLTPPRIYHDAGFGWYKFLICRYTVLFPYANMTYSIVFLGLISIDRYL 141
Db 82 NLATSDTLVLSLPLVLYVADRNWMPGKVFCKVRLFPYANLSSILFLCISVHRM 141
Oy 142 KVVKPGDSRWYSITFKTVLSVCWVIMAVLSLPIIIL--TNGOPTEDNIDHCKLSPL 199
Db 142 GICPIRLSKVYKTHARLILCVGWLVTITCLIPILIVTSSKNSKNSLCHDTTPB--- 198
Oy 200 GVKHTAVTVNS---CLFPAVAVLILIGCIYASIRYIHKSRQFISQSR---RKQNO 252
Db 199 --EFDHVHYASSIMALLFGIPFLVIVVCYCLMARLCK--RSFSPSPRPVSKRSIK 254
Oy 253 SIRVVAVPFTGCELPYHLCRIPFTSHLDRLDEAO--KILYVCKEITLPLSACNVCLD 310
Db 255 MIITLVTFALCPVEFHTR--TLVYSRYFQADCOPLNIIIFYKTIIRPLASINSCLD 311
Oy 311 PIYFPMCRSFRRLFKSNIRTR 334
Db 312 PLYVMADKXRGRLRGAQRPR 335

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RESULT 11

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Oy 08BY11 PRELIMINARY; PRT; 375 AA.
ID 08BY11

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[illegible]

[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Human retina; Mewes H.W., Weill B., Amid C., Oanger A.,
RA Mambert R., Heubner D.,
RA Fodor G., Han M., Wiemann S., EMBL/genbank/DBJ databases.
RL Submitted (JUN-2003) to EMBL
RL EMBL: BX57386; CAD97628.1;
DR Hypothetical protein.
KW SEQUENCE 376 AA; 42720 MW; 7638373C15A695DD CRC64;

Query Match 19.7%; Score 369; DB 4; Length 376;
Best Local Similarity 28.6%; Pred. No. 5, 9e-24; Indels 48; Gaps 10;
Matches 94; Conservative 65; Mismatches 122;

DQ 32 KNTT---LNEDPTIVLPVYLIIFFVSILNLGLAW-IPFHINKTSIFFLKNIIVAD 87
DQ 81 KNATGXYLTSSLSSTLLPAIYLVFVGVPANMVTLMMPFRRSICTVVF-TNLAID 139
DQ 88 LMTLTPPRAYHDAGFGPMYFKTLCKRYSVLEPYAMNSIYFLGISIDRYLKVKRF 147
DQ 140 FLFCVLTPPKIKLYHNGNNWFGVELCATVIYYGNMOSILLACISINRTLATVPLP 199
DQ 148 GDSRKSIPTKYSLSCVVAVMAVLSLPIILNG-----QP---TEDNIGSKLSPFQ 259
DQ 200 TYRGLEPRHYALVTGCVWATVFLMLPEFLIKOEYLVOPDITTCNDVINTCESSPFQ 260
DQ QY 201 VKMTAVTYVNSCLPAVALYILGCYAIISRHYHSKPFIQSRRKANQSIIRVVAV 260
DQ QY 260 LYVISLAFPG---FILPFLIYCCTAAIIRLTNAVDRHL-----WYKASLIIVI 309
DQ QY 261 FTFCEFLPHLCRI---PTFSHLDRLDSDACKILYYCKETFLFSAQNVCDPIITYEF 316
DQ QY 310 FTCPAPSNILTIHHANNYYNNYTDG-----LYFYIALCGISINSCLDPFLYFL 360
DQ QY 317 MCPSFSPRLFKKSNIIRTSSEIRSLOSVR 345
DQ Db 361 MS-----KTRNHSTALTIVK 376

Db 361 MS-----KTRNHSTALTIVK 376

RESULT 13
Q7ZZA4 PRELIMINARY; PRT; 347 AA.
Q7ZZA4
AC Q7ZZA4; (FEB-2003) to the EMBL/GenBank/DBJ databases.
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 25, Last annotation update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE SI:BZ4CJ2.9 (Novel protein similar to nucleotide receptors).
GN Brachydanio rerio (zebrafish) (Danio rerio).
OS Brachydanio rerio (zebrafish); Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Teleostei; Ostariophysi; Cypriniformes;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN (1)
RP SEQUENCE FROM N.A.
RA Struce C.; (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL Submitted
RL EMBL: AL590151; CAD68067.1;
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001884; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:g-protein coupled receptor protein signalin.. .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PS00237; G_PROTEIN_RECIP_F1_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_2; 1.
DR PROSITE: PS02062; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 347 AA; 39861 MW; 3DC01FB3CC283E2 CRC64;

Query Match 19.7%; Score 368.5; DB 13; Length 347;
Best Local Similarity 31.0%; Pred. No. 6, 1e-24; Indels 31; Gaps 11;
Matches 99; Conservative 62; Mismatches 127;

```
QY 35 TLHNEPDTIVLVYLIIFFVASILLGLAWIIF-HIRNKTSFIYLNIVVADLIMLT 93
D 13 TFDSEFKILLPVSLVSLCPGLINSVALMMFTTKMPKSTYVMHLSDLLVLS 72
QY 94 PPRIVHDAGFGPWYFKELCRYSVLFFANMTSIVFLGLISIDRYLKVKVPGDSRMV 153
D 73 LPMIYYAANSNHPFGVVLCKIVRFLFYANLYCSILFLTGISVRYIGICH-----IR 127
QY 154 SITPTK--VLSVC--VWVIAVLSLENIILITNGOPTEDN--IHDCSLKSPGLGVKHTA 206
D 128 SLTLIKPRHAMVCGFWTAVIACLVPTLLVNTSRNNSITLCHDTSRPE-----EFHNP 182
QY 207 VTY---VNSCLFVAVLVILIGYIAISRYIHKSROFI--SOSKRKGNSIRVVAVF 261
D 183 VTNSSVWVWVLFILFELVIVCYCLMARALCOPKRGLANOQSSSRKSKITILVLAVF 242
QY 262 PTCFLPYHLCRIPFTSHDLRLDESAG--KILYYCKEITFLSACNVCLDPIIYFWM-- 317
D 243 AICVPPHITR---TLVYAVRIFPADCKTLNIVNPSYKITRPLASVNSCLDPIIYFLAGD 299
QY 318 -CRSPSRRLFKKSNIRTS 335
D 300 HYRSKLRLVLTROTPTNTRS 318

RESULT 14
Q8NS57 PRELIMINARY; PRT; 339 AA.
AC Q8NS57/
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE G protein-coupled receptor 17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
.OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC031653; AAH31653.1; -.
DR GO: GO:0016021; C:Integral to membrane, IEA.
DR GO: GO:0004872; F:receptor activity, IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity, IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR Interpro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPE_F1_2; 1.
KM Receptor.
SQ SEQUENCE 339 AA; 37860 MW; BBGCAFD0FC371D63 CRC64;

Query Match 18.9%; Score 355; DB 4; Length 339;
Best Local Similarity 30.2%; Pred. No. 8.8e-23;
Matches 95; Conservative 46; Mismatches 124; Indels 50; Gaps 8;
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D 181 ---CLQYREKASHNALVSLVAFTPRITVTCTYLIR-----SLRGLEVREKSKTKKA 233
QY 251 NOSIRVVAVVFTGFLPYHLCRIPFTSHDLRLDESAGKILYYCKEITFLSACNVCLD 310
D 234 VRMIAIVLALFVLVCFVPHVRSYVVLHYRSHGASCATORTIALANRITSLTSLNGALD 293
QY 311 PIIFPFCRSFRRLL 325
D 294 PIMTFVAKFRHAL 308

RESULT 15
Q7ZMO7 PRELIMINARY; PRT; 537 AA.
AC Q7ZMO7/
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
.OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strauberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC046837; AAH46837.1; -.
DR GO: GO:0016021; C:Integral to membrane, IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity, IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR Interpro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPE_F1_2; 1.
KM Hypothetical protein.
SQ SEQUENCE 537 AA; 61981 MW; B030F67D76CB9622 CRC64;

Query Match 18.8%; Score 352; DB 13; Length 537;
Best Local Similarity 31.0%; Pred. No. 2.5e-22;
Matches 95; Conservative 58; Mismatches 133; Indels 20; Gaps 10;
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QY 40 FDTIVLPVLYLIIFFVASILLGLAWIIF-HIRNKTSFIYLNIVVADLIMLTFFPRI 98
D 41 FKFLLPVSVAVMVGGLPNTIAAMWIFIAKGRPMNPPTVYVMFLALSDTLVYSLPVL 100
QY 99 VHDAGFGPWYFKELCRYSVLFFANMTSIVFLGLISIDRYLKVKVPGDSRMVSTFT 158
D 101 YVYADKNMWPGEVLCVRLFYANLYSSILFLTGISVHRYGVCHEPITSLRRNACGA 160
QY 159 KVLSCVAVVIAVLSLENIILITNGOPTEDN--IHDCSLKSPGLGVKHTAVVNSCLF 215
D 161 VVICALVWLSSTLCLVENLIVTVSPKKNATIGCHDTRRBPAPAYVERSTAL---KLL 216
QY 216 VAV-LVILIGCYIAISRYHK--SSRQFISQSRKRKNSIRVVAVFTGFLPYHL 271
D 217 FGICLLIAGCYGAMTRELKMPVYSNGOQLPSYKKSIIKTIIFVMA-LAICFVPHIT 275
QY 272 RIPTFSDHLRLDES--AQKILYYCKEITFLSACNVCLDPIIYFPMCRSPSRRLFKS 329
D 276 R---TLVYVALLGIKCYALVINVTVKTRPLASANSCLDPIIYFLANDRYRRLIR-- 330
QY 330 NITRS 335
D 331 TVRRRS 336

Search completed: June 1, 2004, 15:18:43
Job time : 47 secs
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OM protein - protein search, using sw model

Run on: June 1, 2004, 15:13:14 ; Search time 17 Seconds
(without alignments)
1096.536 Million cell updates/sec

Title: US-09-464-685-1
Perfect score: 1874
Sequence: 1 MGFNLTAKLNENELHGOES.....RSLQSVRSVRVRYDYTDV 358

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1874	100.0	358	1	GP87_HUMAN
2	1731	92.4	358	1	GP87_MOUSE
3	768.5	41.0	338	1	P2YX_HUMAN
4	742.5	39.6	338	1	P2YX_MOUSE
5	700.5	37.4	343	1	P2YX_RAT
6	696	37.1	342	1	P2YC_MOUSE
7	694.5	37.1	342	1	P2YC_HUMAN
8	692.5	37.0	333	1	GP86_HUMAN
9	686.5	36.6	342	1	P2YC_MACFA
10	672.5	35.9	305	1	P2YX_RAT
11	666	35.5	337	1	GP86_MOUSE
12	491.5	26.2	245	1	GP86_MACFA
13	420.5	22.4	319	1	H963_HUMAN
14	376.5	20.1	309	1	CLT2_MOUSE
15	375.5	20.0	342	1	PAPR_CAVPO
16	374	20.0	375	1	GP34_MOUSE
17	372.5	19.9	345	1	CLT2_PIG
18	371.5	19.8	381	1	GP34_HUMAN
19	371.5	19.8	381	1	GP34_PANTR
20	370	19.7	346	1	CLT2_HUMAN
21	368.5	19.7	374	1	PAR3_HUMAN
22	360	19.2	341	1	PAPR_RAT
23	359.5	19.2	369	1	CLT2_RAT
24	358	19.1	367	1	GP17_HUMAN
25	356.5	19.0	341	1	PAPR_MOUSE
26	356.5	19.0	397	1	PAR2_RAT
27	354.5	18.9	368	1	PAR3_RAT
28	352	18.8	537	1	P2Y8_XENTLA
29	349.5	18.6	361	1	P2Y4_RAT
30	349	18.6	399	1	PAR2_MOUSE
31	348.5	18.6	365	1	P2Y4_HUMAN
32	346	18.5	397	1	PAR2_HUMAN
33	345	18.4	361	1	EB12_HUMAN

34	343.5	18.3	361	1	P2Y4_MOUSE	Q9167_mus musculus
35	340.5	18.2	342	1	PAPR_HUMAN	P23105_homo sapien
36	339.5	18.1	340	1	CLT1_PIG	O95n02_sus scrofa
37	334	17.8	337	1	CLT1_HUMAN	O97271_homo sapien
38	333.5	17.8	369	1	PAR3_MOUSE	O08675_mus musculus
39	330.5	17.6	339	1	CLT1_RAT	O92458_rattus norv
40	330	17.6	373	1	P2YR_RAT	P49651_rattus norv
41	329.5	17.6	362	1	P2YR_MELGA	P49652_melagris g
42	329	17.6	373	1	P2YR_CAVPO	P59902_cavia porce
43	328	17.5	362	1	P2YR_CHICK	P34996_gallus gall
44	328	17.5	377	1	P2Y2_HUMAN	P41231_homo sapien
45	327	17.4	363	1	SSRS_RAT	P30938_rattus norv

ALIGNMENTS

RESULT 1
GP87_HUMAN STANDARD: PRT, 358 AA.
ID GP87_HUMAN
AC Q9BY21, Q96J28, Q9BXC2,
DT 10-OCT-2003 (Rel. 42, Created)
DR 10-OCT-2003 (Rel. 42, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DT Probable G protein-coupled receptor GP87.
DE GP87 OR GPR95 OR FKSG78.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Hellbrand S.,
RT "An expressed sequence tag (EST) data mining strategy succeeding in
RL the discovery of new G-protein coupled receptors.",
RN J. Mol. Biol. 307:799-813(2001).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155;
RA Lee D.R., Nguyen T., Lynch K.R., Cheng R., Vancil W.B., Arkhitko O.,
RT Lewis T., Evans J.F., George S.R., O'Dowd B.F.,
RL "Discovery and mapping of ten novel G protein-coupled receptor
RL genes.",
RN Gene 275:83-91(2001).
[3]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Isoqal T., Oca T., Hayaehi K., Sugiyama T., Otaki T., Suzuki Y.,
RT Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
RA Niomiya K., Iwayanagi T.,
RT "New human cDNA sequencing project.",
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
[4]
RP SEQUENCE OF 13-358 FROM N.A.
RX TISSUE=Heart;
RA Wang Y.-G., Gong L.,
RT "Identification of FKSG78, a novel gene encoding a putative G-protein-
RL coupled receptor.",
RN Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
[5]
RP SEQUENCE OF 66-358 FROM N.A.
RX TISSUE=Lung;
RA MEDLINE=22388257; PubMed=12477932;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheiner C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopline R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF293366; AAK01866.1; -;
 DR EMBL; AK080394; BAC37905.1; -;
 DR MGD; MGI:1934133; Gpr87.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008109; P2Y13_Purinocptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PRINTS; PR01735; P2Y13_P2Y13PRNCTR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 68
 FT DOMAIN 69 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 116
 FT TRANSMEM 117 137
 FT DOMAIN 138 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 208
 FT TRANSMEM 209 229
 FT DOMAIN 230 256
 FT TRANSMEM 257 277
 FT DOMAIN 278 297
 FT TRANSMEM 298 318
 FT DOMAIN 319 358
 FT DISULFID 114 192
 FT CARBOHYD 4 4
 FT CARBOHYD 24 24
 FT CARBOHYD 33 33
 FT CONFLICT 1 1
 SQ SEQUENCE 358 AA; 41413 MW; 6D258B98C83BE4B9 CRC64;
 Query Match 92.4%; Score 1731; DB 1; Length 358;
 Best Local Similarity 91.3%; Pred. No. 1.7e-106;
 Matches 327; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

Oy 301 FLGACVCLDPIIYFMCSPSRRLFKSNIRTSSESIRLSQVRSREVIYDYTDV 358
 Db 301 FLGACVCLDPIIYFMCSPSRRLFKSNIRTSSESIRLSQVRSREVIYDYTDV 358
 RESULT 3
 ID P2YX HUMAN STANDARD; PRT; 338 AA.
 AC Q15351;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE UDP-glucose receptor (G protein-coupled receptor GPR105).
 GN GPR105 OR KIAA0001.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP TISSUE=Bone marrow;
 RC MEDLINE=96051387; PubMed=7584026;
 RX Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
 RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
 RT "Prediction of the coding sequences of unidentified human genes. I.
 RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
 RT analysis of randomly sampled cDNA clones from human immature myeloid
 RT cell line KG-1.";
 RL DNA Res. 1:27-35(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21426338; PubMed=11524702;
 RA Joensuu T., Haemeleinen R., Yuan B., Johnson C., Tegelsberg S.,
 RA Gaepariini P., Zelman E., Pirvola U., Pakarinen L., Veenajoki A.-E.,
 RA de la Chapelle A., Sankila B.-M.;
 RT "Mutations in a novel gene with transmembrane domains underlie Usher
 RT syndrome type 3.";
 RL Am. J. Hum. Genet. 69:673-684(2001).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20219108; PubMed=10753868;
 RA Chambers J.K., Macdonald L.E., Sarau H.M., Ames R.S., Freeman K.,
 RA Foley J.J., Zhu Y., McLaughlin M.M., Murdoch P., McMillan L.,
 RA Trill J.J., Swift A., Aiyar N., Taylor P., Vawter L., Milled S.,
 RA Szekeres P., Hervey G., Scott C., Watson J.M., Murphy A.J., Duzic E.,
 RA Klein C., Bergsma D.J., Wilson S., Livi G.P.;
 RT "A G protein-coupled receptor for UDP-glucose.";
 RL J. Biol. Chem. 275:10767-10771(2000).
 CC -1- FUNCTION: Receptor for UDP-glucose and other UDP-sugar coupled to
 CC G-proteins. Not activated by ATP, ADP, UTP or AMP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Highest expression in the placenta, adipose
 CC tissue, stomach and intestine, intermediate levels in the brain,
 CC spleen, lung and heart, lowest levels in the kidney.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; D13626; BA02791.1; -;
 DR EMBL; AF456925; AAL4764.1; -;
 DR Genew; HGNC:16442; GPR105.
 DR GO; GO:0016021; C: integral to membrane; NAS.
 DR GO; GO:0045029; F: UDP-activated nucleotide receptor activity; NAS.
 DR GO; GO:0007186; F: G-protein coupled receptor protein signalin. . .; NAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR005466; UDPG_receptor.
 DR Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PRO0237; GPCRHDOPSN.
DR PRINTS; PRO1655; UDPGLUCOSER.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 29
FT TRANSMEM 30 50
FT DOMAIN 51 55
FT TRANSMEM 56 76
FT DOMAIN 77 96
FT TRANSMEM 97 117
FT DOMAIN 118 139
FT TRANSMEM 140 160
FT DOMAIN 161 188
FT TRANSMEM 189 209
FT DOMAIN 210 234
FT TRANSMEM 235 255
FT DOMAIN 256 278
FT TRANSMEM 279 299
FT DOMAIN 300 338
FT DISULFID 94 172
FT CARBOHYD 3 3
FT CARBOHYD 161 161
SQ SEQUENCE 338 AA; 38971 MW; 8DBE7C782CB4753D CRC64;

Query Match
Best Local Similarity 41.0%; Score 768.5; DB 1; Length 338;
Matches 147; Conservative 64; Mismatches 97; Indels 1; Gaps 1;

QY 44 VLPVYLITFVASILINGIAWIFPHIRNKTSPIFLYKNIVADLIMLTTPPRIVHDAG 103
DB 24 IIPVYICWFIFAGILANGSGWIFPVPSKSGFIYLNKIVADLIMLTTPPRIVHDAG 83
QY 104 RSPWYFKFLCYSTSLFYANNVTSIVELGLSIDRYLVKVPFGDSRWYSTTFKULSV 163
DB 84 LSPWOLNPFVCKVASLFLVNNVTSIVELGLSIDRYLVKVPFGDSRWYSTTFKULSV 143
QY 164 CWMVIMAVLSLPIILITNGOPTEDNIDHDSKSLSPGVGMHTAVTVYNSCLFVAALVILI 223
DB 144 IWMMLMLLAVNIIITLNGSVAEVQIKIEIKSELGRMHKASNYIPAFIMWIFLLI 203
QY 224 GCYIAISRYIHKS-RQFISQSSRRKANQSIKRVAVVFTFGLPYHLCRIFPTSHLDR 282
DB 204 VFYTAITKKIFKSHKSSRNSTSVKKSRIKSFIVFVFCVFEVYHARIPTYSQTEA 263
QY 283 LIDESAOKIYVCKEITLFLSACVNCIDPIITFPMGRSSRLFKKSNRTSESIRSLQ 342
DB 264 HVSCKSKELRYMKETLILSHANVCIDPIITFPMGRSSRLFKKSNRTSESIRSLQ 323
QY 343 SVRSESVRI 351
DB 324 RIKRGNTTL 332

RESULT 4
P2YX_MOUSE STANDARD; PRT; 338 AA.
ID P2YX_MOUSE
AC 09ESG6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE UDP-glucose receptor (G protein-coupled receptor GPR105).
GN GPR105.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN NCB1_TaxID=10090;
RA Lee B.C., Scadden D.T.;
RP "7 transmembrane G protein coupled receptor from hematopoietic
RT progenitors."
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Olfactory epithelium;
RX MEDLINE=22388257; PubMed=12477932.
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for UDP-glucose coupled to G-proteins (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF17211; AACG9275.1; -.
DR EMBL; BC058558; AAH58558.1; -.
DR MGD; MGI:2155705; Gpr105.
DR GO; GO:0016021; C: integral to membrane; ISS.
DR GO; GO:0045029; F: UDP-activated nucleotide receptor activity; ISS.
DR GO; GO:0007186; P: G-protein coupled receptor protein signaln. .; ISS.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR InterPro; IPR005466; UDPG_receptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PRO0237; GPCRHDOPSN.
DR PRINTS; PRO1655; UDPGLUCOSER.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 29
FT TRANSMEM 30 50
FT DOMAIN 51 55
FT TRANSMEM 56 76
FT DOMAIN 77 96
FT TRANSMEM 97 117
FT DOMAIN 118 139
FT TRANSMEM 140 160
FT DOMAIN 161 188
FT TRANSMEM 189 209
FT DOMAIN 210 234
FT TRANSMEM 235 255
FT DOMAIN 256 278
FT TRANSMEM 279 299
FT DOMAIN 300 338
FT DISULFID 94 172
FT CARBOHYD 3 3
FT CARBOHYD 161 161
SQ SEQUENCE 338 AA; 38861 MW; 437650622A684E CRC64;

Query Match
Best Local Similarity 39.6%; Score 742.5; DB 1; Length 338;
Matches 147; Conservative 64; Mismatches 97; Indels 1; Gaps 1;

```

Matches 149; Conservative 67; Mismatches 116; Indels 7; Gaps 3;

QY 22 NSGRSDPGKNTLHNEFDIVLPVLYLLIFVASILNGLAVWFFHIRKTSIFPYLK 81
 DB 2 NNSSTTDPNPPCSNNTLITKQIIPVLGWFITGLNLNGISGMFFVPPSSKSFITLK 61

QY 82 NIVVADIMLTLPFPRIIVHDAGFGPMYFKILCRYSVLFPANNYSIVFLGLISIDRYL 141
 DB 62 NIVVADIMLTLPFPRIIVHDAGFGPMYFKILCRYSVLFPANNYSIVFLGLISIDRYL 121

QY 142 KVVXKPGDSRMYSITFTKVLVSCVWVIMAVLSLPIIILITNGQPEDNINHCSKLSPLGV 201
 DB 122 KIVKPLSLTISIVQSVNSKLSVLVWMLMLLAVPNIILITNGQVEVTKIQCEHLEINELGR 181

QY 202 KMTAVTVVNSCLFPAVLVILIGCIYASRYIHKS---SRQFISGSSRRKRNQSIIRVV 258
 DB 182 KMHKSNYIFVSIFFVWVLLIVFYATITRKIFKHLKSRK--NSTSVKRSNRIFSIIV 239

QY 259 AVFPTCFPLPHLCRIPTFFSHLDRLDLSAQKILYCKEITLFLSACVNCCLDPIIYFPMC 318
 DB 240 LVFVVCFFVPHIARIPTKSGTEGHSQRTKETLILYAEFTLLLSAANVCDDPIIYFPLC 299

QY 319 RSPFRRLPKSGNIRTRSESIRSLQSVRSSEVRIYYDITD 357
 DB 300 QPFREVLNKLMHSLKQNDLEVSRTKRENA--IHESITD 336

RESULT 5
 P2YC_RAT STANDARD; PRT; 343 AA.

AC Q9CPK4;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=21037966; PubMed=1196645;
 RA Hollinger G., Jentzen H.-M., Vincent D., Li G., England L.,
 RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,
 RA Conley P.B.;
 RT "Identification of the platelet ADP receptor targeted by
 RT antithrombotic drugs";
 RL Nature 409:202-207(2001).
 CC -1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
 CC inhibit the adenylyl cyclase second messenger system (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; AF134450; AAG48945.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR005394; P2Y12_purinoceptor.
 DR Pfam; PF00001; Gtm_1; 1
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PRINTS; PR01569; P2Y12_PNCPTR.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
 DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 32 52 1 (POTENTIAL).
 FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 65 85 2 (POTENTIAL).
 FT DOMAIN 86 105 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 106 126 3 (POTENTIAL).
 FT DOMAIN 127 148 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 149 169 4 (POTENTIAL).
 FT DOMAIN 170 197 5 (POTENTIAL).
 FT TRANSSEM 198 218 6 (POTENTIAL).
 FT DOMAIN 219 239 7 (POTENTIAL).
 FT TRANSSEM 240 260 6 (POTENTIAL).
 FT DOMAIN 261 287 7 (POTENTIAL).
 FT TRANSSEM 288 308 7 (POTENTIAL).
 FT DOMAIN 309 343 CYTOPLASMIC (POTENTIAL).
 FT DISULFD 103 181 BY SIMILARITY.
 FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 12 12 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 343 AA; 39047 MW; 7AE0AFCE6674136 CRC64;

Query Match 37.4%; Score 700.5; DB 1; Length 343;
 Best Local Similarity 43.8%; Pred. No. 3.4e-39;
 Matches 134; Conservative 66; Mismatches 103; Indels 3; Gaps 2;

QY 23 NSGRSDPGKNTLHNEFDIVLPVLYLLIFVASILNGLAVWFFHIRKTSIFPYLK 80
 DB 10 SANTTSIPGISTLSRDKYKIQVLPFLYTLVFPAGLITNSLAWRIFQHSKSFIFL 69

QY 81 KNIVADIMLTLPFPRIIVHDAGFGPMYFKILCRYSVLFPANNYSIVFLGLISIDRY 140
 DB 70 KNIVADIMLTLPFPRIIVHDAGFGPMYFKILCRYSVLFPANNYSIVFLGLISIDRY 129

QY 141 LKVVKPGDSRMYSITFTKVLVSCVWVIMAVLSLPIIILITNGQPEDNINHCSKLSPLG 200
 DB 130 LKVVKPGDSRMYSITFTKVLVSCVWVIMAVLSLPIIILITNGQPEDNINHCSKLSPLG 189

QY 201 VKMTAVTVVNSCLFPAVLVILIGCIYASRYIHKS---SRQFISGSSRRKRNQSIIRVV 259
 DB 190 LVHMEIVNYIQVLFNINFLIVICYSILITELVRSYRTGSAKAPKRNINIKFIIIA 249

QY 260 VFPTCFPLPHLCRIPTFFSHLDRLDLSAQKILYCKEITLFLSACVNCCLDPIIYFPMC 319
 DB 250 VFPTCFPLPHLCRIPTFFSHLDRLDLSAQKILYCKEITLFLSACVNCCLDPIIYFPMC 309

QY 320 SFSRRL 325
 DB 310 SFSRNSL 315

RESULT 6
 P2YC_MOUSE STANDARD; PRT; 347 AA.

AC Q9CPV9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE P2Y purinoceptor 12 (P2Y12).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus, and Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamaneke I.,
 RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli P., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarrelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Wilmberg L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuke S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Marz M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
inhibit the adenylyl cyclase second messenger system (By
similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL, AK013804; BAB29000.1; -
CC EMBL, AK014807; BAB29561.1; -
CC EMBL, BC025428; AAH25428.1; -
CC EMBL, BC027381; AAH27381.1; -
CC MGD, MGI:1918089; P2ry12.
DR GO, GO:0005887; C: integral to plasma membrane; IC.
DR GO, GO:0001609; P: adenosine receptor activity; G-protein coupled; IMP.
DR GO, GO:0001621; P: platelet ADP receptor activity; IMP.
DR GO, GO:0007188; P: G-protein signaling; coupled to cAMP nucleo. . .; IMP.
DR GO, GO:0030168; P: platelet activation; IMP.
DR InterPro, IPR000276; GPCR_Rhodopsin.
DR InterPro, IPR005394; P2ry12_purinoceptor.
DR Pfam, PF00001; 7tm.1.1.
DR PRINTS, PR00237; GPCR_Rhodopsin.
DR PRINTS, PR01569; P2ry12_P2ry12.
DR PROSITE, PS00237; G_PROTEIN_RECEP_F1_1; FALSE NEG.
DR PROSITE, PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; glycoprotein.
FT DOMAIN 1 31
FT TRANSMEM 32 52
FT DOMAIN 53 64
FT TRANSMEM 65 85
FT DOMAIN 86 105
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 106 126
FT DOMAIN 127 148
FT TRANSMEM 149 169
FT TRANSMEM 170 197
FT TRANSMEM 198 219
FT TRANSMEM 219 239
FT TRANSMEM 240 260
FT TRANSMEM 261 287
FT TRANSMEM 288 308
FT TRANSMEM 309 347
FT DISULFID 103 181
FT CARBOHYD 7 7
FT CARBOHYD 12 12
FT CONFLICT 3 3
SQ SEQUENCE 347 AA; 39473 MW; F1074885E7B025F1 CMC64;
Query Match 37.1%; Score 696; DB 1; Length 347;
Best Local Similarity 43.3%; Pred. No. 6.7e-39;
Matches 136; Conservative 61; Mismatches 101; Indels 16; Gaps 2;
QY 28 DQPGNTTLN-----EEDTIVLVYLIIFVASILNGLAVMFPHIRN 72
DB 2 DVGAVNTTSANTTSPGISTLCVADYKLTQVLFPLVTVLFAGLITSLMRIFFOIRS 61
QY 73 KTSFFLYKNIVADLMTLTPPRIVADAGCPWFYFELICRYTSVLFYANMTSYFL 132
DB 62 KSNFIFLKNIVISDLMLTFPKLISDALGAGPRLTVCQVTSVTFYTWISISFL 121
QY 133 GLISIDRYLKVKPGDSRMYSITFYKLVSCVAVINAVLSLPIILITNGOPTEDNIDC 192
DB 122 GLITIDRYLKTTRPKTSSPENLGAKLISVIAWAFELSLPMNITLNRPRKDKVVC 181
QY 193 SKLSPGVKMHVATVYNSCLFVAVLVILIGCIATISRYHRS-SPOFISQSRKKHN 251
DB 182 SPLSEFSLVHSELVNVIQVYFVNFIVVCSLTTELKRYRYVTRGSAKPKKKVN 241
QY 252 QSRVAVAFPTCELPYHLCRIPTFSDRLDESAOKILYCKEITLPLACNVCLDP 311
DB 242 VKVFIILAVFICVPHFPAIPIYTLTQTRAVFPCSAENTLFYKKESTWITSNACIDP 301
QY 312 IYFPMCRSFRRL 325
DB 302 FIVEFLCKSFNSL 315
RESULT 7
P2YC_HUMAN STANDARD; PRT; 342 AA.
AC Q9H244;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor) (P2Y (ADP))
DE (ADP-glucose receptor) (ADPG-R) (P2Y (AC)) (P2Y (cyc)) (P2Y (AC))
DE (SP1999).
GN P2RY12 OR HOKR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RN SEQUENCE FROM N.A.
RX MEDLINE=21037966; PubMed=11196645;
RA Hollopeter G., Jantzen H.-M., Vincent D., Li G., Englund L.,
RA Ramakrishnan V., Yang R.-B., Nudsen P., Nudsen A., Julius D.J.,
RA Conley P.B.,
RT "Identification of the platelet ADP receptor targeted by
antithrombotic drugs.";
RL Nature 409:202-207(2001).
RN 12
RN SEQUENCE FROM N.A.
RP TISSUE=Hypothalamus;
RC MEDLINE=21269433; PubMed=11104774;
FT

RA Zhang F.L., Luo L., Gustafsson E., Iachowicz J., Smith M., Qiao X.,
 RA Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,
 RA Monma F.J. Jr.,
 RT "ADP is the cognate ligand for the orphan G protein-coupled receptor
 RT SP199.";
 RT J. Biol. Chem. 276:8608-8615(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21394281; PubMed=11502873;
 RA Takasaki J., Kamahara M., Saito T., Matsumoto M., Matsumoto S.-I.,
 RA Ohishi T., Soga T., Matsumoto H., Furuchi K.;
 RT "Molecular cloning of the platelet P2U(AC) ADP receptor:
 RT pharmacological comparison with another ADP receptor, the P2Y1
 RT receptor.";
 RT Mol. Pharmacol. 60:432-439(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Relascheid R.K., Nothacker H.-P., Wang Z., Zeng J., Ehler F.J.,
 RA Civealli O.;
 RT "ADP-glucose activates a G-protein coupled receptor and inhibits
 RT smooth muscle contractions.";
 RT Submitted (Oct-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040266; PubMed=12044878;
 RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
 RT "Identification of G protein-coupled receptor genes from the human
 RT genome sequence.";
 RT FEBS Lett. 520:97-101(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RT Submitted (Jul-2002) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Kleisner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.B.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rahn S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pailey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.T., Skalska U., Smalios D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
 CC inhibit the adenylyl cyclase second messenger system. Not
 CC activated by UDP and UTP. Involved in platelet aggregation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in the platelets, lower
 CC levels in the brain, lowest levels in the lung, appendix,
 CC placenta and adrenal gland. Expressed in the spinal cord and in
 CC the fetal brain.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 DR EMBL; AF313449; AAC48944.1; -
 DR EMBL; AF313815; AAK09948.1; -
 DR EMBL; AB052664; BAB60824.1; -
 DR EMBL; AF310665; AAL32292.1; -
 DR EMBL; AB083596; BAB9309.1; -
 DR EMBL; AY136754; AAN01280.1; -
 DR EMBL; BC017898; AAL17898.1; -
 DR Genem; HGNC:18124; P2RY12.
 DR MIM; 600515; -
 DR GO; GO:0016020; C:membrane; NAS.
 DR GO; GO:0070599; P:hemostasis; NAS.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR005394; P2Y12_purinocptor.
 DR InterPro; IPR008109; P2Y13_purinocptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PRINTS; PR01569; P2Y12_P2RY12.
 DR PRINTS; PR01735; P2Y13_P2RY12.
 DR PROSITE; PS00237; G-PROTEIN_RECPT_F1_1; FALSE_NEG.
 DR PROSITE; PS00262; G-PROTEIN_RECPT_F1_2; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECPT_F1_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 25
 FT TRANSMEM 26 46
 FT DOMAIN 47 58
 FT TRANSMEM 59 79
 FT DOMAIN 80 99
 FT TRANSMEM 100 120
 FT DOMAIN 121 142
 FT TRANSMEM 143 163
 FT DOMAIN 164 191
 FT TRANSMEM 192 212
 FT DOMAIN 213 233
 FT TRANSMEM 234 254
 FT DOMAIN 255 281
 FT TRANSMEM 282 302
 FT DOMAIN 303 342
 FT DISULFID 97 175
 FT CARBOHYD 6 6
 FT CARBOHYD 13 13
 SQ SEQUENCE 342 AA; 39438 MW; 8553D2746C89176D CRC64;
 Query Match 37.1%; Score 694.5; DB 1; Length 342;
 Best Local Similarity 42.2%; Pred. No. 8.3e-39;
 Matches 139; Conservative 68; Mismatches 113; Indels 9; Gaps 5;
 QY 25 NRSDDGKNTLL--HNEFDIVLVLVLIIFVASILNGLAWIFPHIRKTSIFYLK 81
 DB 6 NLTSAPG-NTSLCTRDYKITQVLPFLVTVFVGLTLNGLAMRIFFOIRSKSNFIIFLK 64
 QY 82 NIVVADILMTLTPRPRIYHDAGFGWYFKFLICRTSYLFPANWTSIVPGLSIDRYL 141
 DB 65 NTVISDLMILTPPKLISDKLGGPRTVCQVTSVIFFTWISISFGLITIDRQ 124
 QY 142 KVVKPGDSRWYSIFTFVLISVCVWIVAVLSPIIILTNQPTEDNIDSKSLPGLV 201
 DB 125 KTRPRFKTSKNKLLGAKILSVIWFAPLSTPLMLITNQPRKNVKKSFLLSEFGL 184
 QY 202 KMTAVTVYNSCLFAVLVILGCIYAIASRYHKS--SRQFISQSSRRKKNQSIKRVVA 259
 DB 185 VMHEIVNYICQVIFINFLIYVCTLLTKELYSYVTRGVGKPRK-KVNVKVFIIIA 243
 QY 260 VFFGCELPYHCRIPFTFSHDLRLDSAQKILYVCKEITLPLASNCVCLDPIIYFPCR 319
 DB 244 VFFICEVFHARIPYLTLSQTRDVFDCYAEWTLTFVKSSTLMTLSLNAKDLPIYFLCK 303
 QY 320 SFSRRLFFKSNIRTSBSIRLSQVRSE 348

Db 304 SFRNSLI--SMKCPNATSLSQDNKKE 330

RESULT 8

ID GPR86 HUMAN STANDARD; PRT; 333 AA.

AC GPR86; Q81UT5; Q82DU7;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Probable G protein-coupled receptor GPR86 (P2Y purinoceptor 13) (P2Y13).

DE GPR86 OR GPR94 OR FKSG77.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCB1_TaxID=9606;

OX [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Amalgala, Caudate, Fetal brain, and Placenta;

RX MEDLINE=21172992; PubMed=11273702;

RA Wittenberger T., Schaller H.C., Heilebrand S.,

RT "An expressed sequence tag (EST) data mining strategy succeeding in the discovery of new G-protein coupled receptors.";

RL J. Mol. Biol. 307:799-813 (2001).

[2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21458557; PubMed=11574155;

RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arhitek O., Lewis T., Evans J.F., George S.R., O'Powd B.F.;

RT "Discovery and mapping of ten novel G protein-coupled receptor genes.";

RL Gene 275:83-91 (2001).

[3]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=21538899; PubMed=11546776;

RA Communi D., Gonzalez N.S., Dethieux M., Brezillon S., Lannoy V., Parmentier M., Boeynaems J.M.,

RT "Identification of a novel human ADP receptor coupled to Gi.";

RL J. Biol. Chem. 276:41479-41485 (2001).

[4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22040266; PubMed=12044878;

RA Takada S., Kadowaki S., Haga T., Takeasu H., Mitaku S.;

RT "Identification of G protein-coupled receptor genes from the human genome sequence.";

RL FEBS Lett. 520:97-101 (2002).

[5]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX Wang Y.-G., Gong L.;

RT "Molecular cloning of FKSG77, a novel gene encoding a putative G-protein-coupled receptor.";

RL Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.

[6]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Straube R.L., Felting E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J., Boeck S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hultik S.W., Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.;

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherich A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- FUNCTION: Orphan receptor. Seems to be a G(i)-coupled receptor displaying a high affinity for ADP. Might play a role in hematopoiesis and the immune system.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Strong expression in spleen and adult brain. Lower expression in placenta, lung, liver, spinal cord, thymus, small intestine, uterus, stomach, testis, fetal brain, and adrenal gland. Not detected in pancreas, heart, kidney, skeletal muscle, ovary or fetal aorta. Clearly detected in lymph node and bone marrow, weakly detected in peripheral blood mononuclear cells (PBMC) and in peripheral blood leukocytes (PBL), but not detected in polymorphonuclear cells (PMN). In the brain, detected in all brain regions examined.

CC -1- MISCELLANEOUS: Stimulation by ADP in stably transfected CHO cells resulted in inhibition of adenylyl cyclase and the phosphorylation of the MAP kinases MAPK3 and MAPK1 in a pertussis toxin-sensitive way. Inhibition of adenylyl cyclase and phosphorylation of the MAP kinases are transduction mechanisms that involve G(i) proteins.

CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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CC -----

CC EMBL; AF295368; AAK01864.1; -

CC EMBL; AF411113; AAL26484.1; -

CC EMBL; AF406692; AAL01038.1; -

CC EMBL; AB083597; BAB89310.1; -

CC EMBL; AF345565; AAK29068.1; -

CC EMBL; BC041116; AAK41116.2; -

CC GeneW; HGNC:4537; GPR86.

CC MIM; 606380; -

CC GO; GO:0016021; C:Integral to membrane, NMS.

CC GO; GO:0016526; F:G-protein coupled receptor activity, unknown. . . ; NAS.

CC InterPro; IPR000276; GPCR Rhodopsin.

CC InterPro; IPR008109; P2Y12_purinocptor.

CC Pfam; PF00001; 7tm_1; 1.

CC PRINTS; PR00237; GPCR_Rhodopsin.

CC PRINTS; PR01735; P2Y13_Rhodopsin.

CC PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.

CC PROSITE; PS50262; G-PROTEIN RECP_F2_1; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein.

CC DOMAIN 1

FT TRANSSEM 1 28

FT DOMAIN 1 49

FT TRANSSEM 50 56

FT DOMAIN 57 77

FT TRANSSEM 78 96

FT DOMAIN 97 117

FT TRANSSEM 118 140

FT TRANSSEM 141 161

FT DOMAIN 162 190

FT TRANSSEM 191 211

FT DOMAIN 212 231

FT TRANSSEM 232 252

FT DOMAIN 253 279

FT TRANSSEM 280 300

FT DOMAIN 301 333

FT TRANSSEM 333 353

FT DISULFID 95 173

FT CARBOHYD 2 2

FT CARBOHYD 10 10

FT CARBOHYD 264 264

FT CONFLICT 158 158

FT SEQUENCE 333 AA; 38440 MW; F234ABBS0016DF34 CRC64;

Db 6 VCRSLSVFVETMYGVILGLIADRFLKIIRLRNIFLKKTVAQTVSVFMSFFFI 65
 Qy 173 SLPLIILNGOPTEDNIHDCSKLSPGLGVKHTAVTVNSCLFVAVILIGCIATISRY 232
 Db 66 SLPLMILNKETAPSSVKKCASLKGPDGLKMHQIVNNISQIFWIVFVLMVFYVIAKK 125
 Qy 233 IHKSSROFISOSRRKKNQSR----VVAVVFPCFIPYHLCRIPEFESHDLRLDLSA 288
 Db 126 VYDSYRRK--SKSKRKNNKKLEKGVFVAVVAFVCFAPFHTRVYVYSQTNNKTQRL 182
 Qy 289 OKILYCKEITLFLSACNVCLDPIIYFPMCSFSRRL 325
 Db 183 QNQLFIACKETLFLAATNINCDPLIYFLCKKFTKRL 219

RESULT 13
 ID_H963_HUMAN STANDARD; PRT; 319 AA.
 OI4626;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable G protein-coupled receptor H963.
 GN H963.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral blood monocytes;
 RX MEDLINE=98036061; PubMed=9370294;
 RA Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M.,
 RA Golden-Fleet M., Kelleher K., Kriz R., Lavallie E.R., Metberg D.,
 RA Spaulding V., Stover J., Williamson M.J., McCoy J.M.;
 RT "A genetic selection for isolating cDNAs encoding secreted proteins.",
 RL Gene 198;289-296(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21426338; PubMed=11524702;
 RA Joensuu T., Haemaelaenen R., Yuan B., Johnson C., Tegelberg S.,
 RA Gaspardini P., Zeleante L., Pirvola U., Pakarinen L., Lehesjoki A.-E.,
 RA de la Chapelle A., Sankila A.-M.;
 RT "Mutations in a novel gene with transmembrane domains underlie Usher
 syndrome type 3.",
 RL Am. J. Hum. Genet. 69:673-684(2001).
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 CC EMBL: AF002986; AAC51846.1; -;
 CC EMBL: AF411849; AAL47763.1; -;
 CC GO: GO:0016021; C:integral to membrane; NAS.
 CC GO: GO:0004930; F:G-protein coupled receptor activity; NAS.
 CC GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm_1.1.
 CC PRINTS: PR00237; GPCR_RHODOPEN.
 CC PROSITE: PS00337; G-PROTEIN RECP F1.1; 1.
 CC PROSITE: PS00262; G-PROTEIN RECP F1.2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 21
 FT TRANSMEM 22 42
 FT DOMAIN 43 48
 FT TRANSMEM 49 69
 FT TRANSMEM 2 (POTENTIAL).
 FT TRANSMEM 2 (POTENTIAL).

FT DOMAIN 70 89
 FT TRANSMEM 90 110
 FT DOMAIN 111 132
 FT TRANSMEM 133 153
 FT DOMAIN 154 181
 FT TRANSMEM 182 202
 FT DOMAIN 203 224
 FT TRANSMEM 225 245
 FT DOMAIN 246 268
 FT TRANSMEM 269 289
 FT DOMAIN 290 319
 FT CARBOHYD 3
 FT SEQUENCE 319 AA; 36754 MM; 79B9821C10841114 CRC64;

Query Match 22.4%; Score 420.5; DB 1; Length 319;
 Best Local Similarity 25.6%; Pred. No. 6.1e-21;
 Matches 83; Conservative 64; Mismatches 126; Indels 7; Gaps 3;

Qy 49 YLIIFVASILNLGAVWVIFPHIR-NKTSFIFYLKNIVADLIMLTFFPFRIVHDAGGPW 107
 Db 21 FYLVFLVGLIISCRATWAFIQKNNHCVSILNLTLADRLTLALPVKIVVDLGVAPW 80
 Qy 108 YKFKILCRYGVLFYANNYTSIVFLGLISDRYLKVVKPFQDSNYSITFKVLSVCVW 167
 Db 81 KLKTFHCQVTFACLIYIMMYLSIIFLAFVSIDRCQLTHSCKIVRIQBFQAKMSTVWL 140
 Qy 168 IMAVLSLPLIILNGOPTEDNIHDCSKLSPGLGVKHTAVTVNSCLFV-AVAVILIGC 225
 Db 141 MWLLIMVPMNMTIPKIDIKESNVGMEPKKEFGNNMLNLFVAILFNSAIIILSN 200
 Qy 226 YIAISRYIHKSSROFISOSRRKKNQSRVVAVVAFVCFAPFHTRVYVYSQTNNKTQRL 285
 Db 201 LVINQLVRNNKNENY----PVKKALINILVTGYILCEPVYIVIPYLSQTEVITD 256
 Qy 286 ESAOKILYCKEITLFLSACNVCLDPIIYFPMCSFSRRL 325
 Db 257 CSTRISLFRKAEATVLLAVSNLCFDPILYHLSKAFRSKV 296

RESULT 14
 ID_C172_MOUSE STANDARD; PRT; 309 AA.
 AC Q920A1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteinyll leukotriene receptor 2 (CysLTR2).
 GN CysLTR2 OR CYSLTR2.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=21601669; PubMed=11591709;
 RA Hui Y., Yang G., Galiczenski H., Figueroa D.J., Austen C.P.,
 RA Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.P.;
 RT "The murine cysteinyl leukotriene 2 (CysLTR2) receptor. cDNA and
 RT genomic cloning, alternative splicing, and in vitro
 RT characterization.",
 RL J. Biol. Chem. 276:47489-47495(2001).
 CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
 CC mediated via a G-protein that activates a phosphatidylinositol-
 CC calcium second messenger system. The rank order of affinities for
 CC the leukotrienes is LTC4 = LTD4 >> LTE4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed at low levels, with highest
 CC expression in the spleen, thymus and adrenal gland, and lower in
 CC the kidney, brain and peripheral blood leukocytes.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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CC EMBL AF31658: AAK97354.1; -
 DR MGD; MGI:1917336; Cyb1t2.
 DR GO; GO:0016020; C:membrane; IDA.
 DR GO; GO:0001631; F:cyteineyl leukotriene receptor activity; IDA.
 DR InterPro; IPR004071; Cyaleuk_receptor.
 DR InterPro; IPR002761; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7cm1; 1.
 DR PRINTS; PR001533; CTSITRECPTR.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 26
 FT TRANSMEM 1 26
 FT DOMAIN 27 47
 FT TRANSMEM 48 56
 FT DOMAIN 57 77
 FT TRANSMEM 78 98
 FT TRANSMEM 99 119
 FT DOMAIN 120 138
 FT TRANSMEM 139 159
 FT DOMAIN 160 187
 FT TRANSMEM 188 208
 FT DOMAIN 209 229
 FT TRANSMEM 230 250
 FT DOMAIN 251 271
 FT TRANSMEM 272 292
 FT DOMAIN 293 309
 FT DISULFID 95 171
 FT CARBOHYD 14 14
 SQ SEQUENCE 309 AA; 35227 MW; 327B14A6BDDDA02 CRC64; (POTENTIAL).

Query Match 20.1%; Score 376.5; DB 1; Length 309;
 Best Local Similarity 31.2%; Pred. No. 4,5e-18;
 Matches 101; Conservative 56; Mismatches 134; Indels 33; Gaps 12;

QY 23 SGNSSDGGKNTLNEFDIVLPVLYLIFVASILNGLAWIFPHI-IRNKTSPFIPLK 81
 DB 4 TGTBSSYNRNCTIEN-FKKEPPIYIILIFPGALNGFSLVYLQTCCKSTSVNVFML 62
 QY 82 NIIVVADLIMTLTLPFRIVHDAGFGPMYKFLICRTSVLFYANMTYSIVFLGLSIDRYL 141
 DB 63 NLATSDFLFISTLPPRADYIPRGSNWIIFODLACRMWSISLVNMTYSITFLVLSVARFQ 122
 QY 142 KVVKPFSGDSRMYSITFTK--VLSVCVWVIMAVLSLPNIIITNGOPTEDNIHDC----S 193
 DB 123 ATVHPF--RMPHVTVSRSAMILGIIWVF--IMASSALLLVNGEKNIIISCLSLSPQ 177
 QY 194 KLSKSLGKMTYAVYVNSCLFVAVALVILICGYIASIRYIKHSNQFISQSRRKKHNS 253
 DB 178 KFKSL-LIMNHIAV--AVGFLPLFLTYCYLIILILKAE--IPESGPRAHAKKA 229
 QY 254 IRVVV--AVFPTCLPYHLICRIPTFSHLDRLLDESOKILYCKEITLFLSACNVCLD 310
 DB 230 LTTIVIAMITPLCLPLPHALRT-----LHLVTWMDSCGDVIAKRVITITLMAANSNCFN 285
 QY 311 PIYIFMCRSPFRRL--PKKSN 331
 DB 286 PFLYFAGENFKARLRAIFSKVL 309

RESULT 15
 PAIR_CAVPO STANDARD; PRT; 342 AA.
 ID PAIR_CAVPO
 AC P21556;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Platelet activating factor receptor (PAF-R).

GN PAFR.
 OS *Cavia porcellus* (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 CX NCBI_Taxid=10141;

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
 RX MEDLINE=91101726; PubMed=1846231;
 RA Honda Z.-I., Nakamura M., Miki I., Minami M., Watanabe T., Seyama Y.,
 RA Okada H., Toh H., Ito K., Miyamoto T., Shinzui T.;
 RT "Cloning by functional expression of platelet-activating factor
 RT receptor from guinea-pig lung.";
 RL Nature 349:342-346 (1991).

CC -1- FUNCTION: Receptor for platelet activating factor, a chemotactic
 CC phospholipid mediator that possesses potent inflammatory, smooth-
 CC muscle contractile and hypotensive activity. Seen to mediate its
 CC action via a G protein that activate a phosphatidylinositol-
 CC calcium second messenger system.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL, X56736; CA440060.1; -
 DR PIR; S13638; S13638.
 DR InterPro; IPR002761; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7cm1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.

FT DOMAIN 1 16
 FT TRANSMEM 17 38
 FT DOMAIN 39 54
 FT TRANSMEM 55 74
 FT DOMAIN 75 91
 FT TRANSMEM 92 113
 FT DOMAIN 114 133
 FT TRANSMEM 134 155
 FT DOMAIN 156 184
 FT TRANSMEM 185 205
 FT DOMAIN 206 233
 FT TRANSMEM 234 254
 FT DOMAIN 255 276
 FT TRANSMEM 277 296
 FT DOMAIN 297 342
 FT CARBOHYD 4 4
 FT CARBOHYD 169 169
 FT DISULFID 90 173
 SQ SEQUENCE 342 AA; 38984 MW; B6413B3A5C87B175 CRC64;

Query Match 20.0%; Score 375.5; DB 1; Length 342;
 Best Local Similarity 27.2%; Pred. No. 5.7e-18;
 Matches 96; Conservative 74; Mismatches 148; Indels 35; Gaps 9;

QY 22 NSGNRSDGKNTLNEFDIVLPVLYLIFVASILNGLAWIFPHI--RNKTSPIF 78
 DB 4 NSSSRVD-----SEFRITLPIYISIIIFVGLIANGVAVNVPALRYSKLNEIKI 54
 QY 79 YLKIIVVADLIMTLTLPFRIVHDAGFGPMYKFLICRTSVLFYANMTYSIVFLGLSID 138
 DB 55 FMNVLTIVADLILTLTLPMTIYVYNSQGWFLPKFLCNLAGLFLPINTYCSVAFLGVITYN 114

```

Oy 139 YLLKVKVKGPGDSRMYSITFTKXLSVCVWYIM-----VLSPIIILNMGCTEDNIHD 191
Db 115 RFOAKYKPKTKYQOATTRKRGIALSLTVAIYAAASFYLMOSTNVV--SNKAGSGNITR 172
Oy 192 CSKLKSLPGVKMHTAVTYVNSCL--FVAVLVYLICCYIAISRYIHKSRSFOPISQSR-- 246
Db 173 CPENYE---KSKPVLIIHICIVLGFIVELLITFCNLYI---IHTLRQPKQORNAE 225
Oy 247 -KRKNHQSIRVVVAVPFCTFLRYHLGRIFFTSBHDRLRLDESAOKLIYKKEITLPLSAC 305
Db 226 VRRRLIMWCYLAFAVLCFVPHHWOLPWTLLAELG-MPSSNHQAINDAHQVTLCLIST 284
Oy 306 NVCLDPIIYFPMCRSFSRLPKFSNIRTRSEGISRISQSVARSEVRIYYDDTDV 358
Db 285 NCVLDPIVICYFLTKKFKRLSEKDLNMRSSQKSRVTTDGTGEMALPIINHTPV 337

```

Search completed: June 1, 2004, 15:17:44
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: June 1, 2004, 15:11:49 ; Search time 58 Seconds
(without alignments) 1744.000 Million cell updates/sec

Title: US-09-464-685-1

Perfect score: 1874

Sequence: 1 MGFLTLAKLPNNELHGES.....RSLQSVRSVRIVYDTRDV 358

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_29Jan04:*

1: Geneseqp1980a:*\n2: Geneseqp1990a:*\n3: Geneseqp2000a:*\n4: Geneseqp2001a:*\n5: Geneseqp2002a:*\n6: Geneseqp2003a:*\n7: Geneseqp2003bs:*\n8: Geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1874	100.0	358	AA45039	AA45039 Human G p
2	1874	100.0	358	AA44365	AA44365 Human G-p
3	1874	100.0	358	AA83014	AA83014 Human G p
4	1874	100.0	358	AA89684	AA89684 Human nov
5	1874	100.0	358	AA60319	AA60319 Human G-p
6	1874	100.0	358	AA67484	AA67484 Amino aci
7	1874	100.0	358	AA84820	AA84820 Human bla
8	1874	100.0	358	ABUS6683	ABUS6683 Lung canc
9	1874	100.0	358	ABR01795	ABR01795 Human can
10	1874	100.0	358	ABP81966	ABP81966 Human G p
11	1874	100.0	358	ABU09897	ABU09897 Human G-p
12	1874	100.0	358	AAE34531	AAE34531 Human Mow
13	1874	100.0	358	AAE34534	AAE34534 Human Mow
14	1874	100.0	358	AAE34533	AAE34533 Human Mow
15	1871	99.8	358	AA85890	AA85890 Human C-P
16	1871	99.8	358	AA894659	AA894659 Human pro
17	1867	99.6	358	AAE02499	AAE02499 Human CON
18	1863.5	99.4	358	ABUS6480	ABUS6480 Lung canc
19	1855	99.0	384	AA884205	AA884205 Amino aci
20	1846	98.5	358	AA282820	AA282820 Human G-p
21	1846	98.5	358	ABG77171	ABG77171 Prostate
22	1846	98.5	358	ABUS7629	ABUS7629 Different
23	1846	98.5	358	ADC33516	ADC33516 Human G p
24	1840	98.2	358	AA860692	AA860692 Human G p
25	1731	92.4	358	AAE34532	AAE34532 Mouse Mow

26	1685	89.9	346	AAE34535	AAE34535 Human Mow
27	889	47.4	196	ABB90283	ABB90283 Human pol
28	768.5	41.0	338	AAV58237	AAV58237 Human KIA
29	768.5	41.0	338	AAE04388	AAE04388 Human UDP
30	768.5	41.0	338	AAU84287	AAU84287 Human end
31	768.5	41.0	338	ABB80778	ABB80778 Human ace
32	768.5	41.0	338	ABP81864	ABP81864 Human UDP
33	768.5	41.0	338	ADC35172	ADC35172 Human GPR
34	768.5	41.0	338	ADC35525	ADC35525 Human KIA
35	768.5	41.0	338	ADG62976	ADG62976 Human Pro
36	762.5	40.7	325	ABU63239	ABU63239 Human G-p
37	742.5	39.6	338	AAV94270	AAV94270 Mouse 7-t
38	742.5	39.6	338	ABB80779	ABB80779 Mouse ace
39	735.5	39.2	338	AAV97541	AAV97541 Rat KIAA0
40	703.5	37.5	333	ADC55385	ADC55385 Human pur
41	700.5	37.4	343	AAE04384	AAE04384 Rat P2-pu
42	700.5	37.4	343	ABP70856	ABP70856 Rat P2T r
43	696	37.1	347	AA48354	AA48354 Murine G
44	696	37.1	347	ABP70855	ABP70855 Murine P2
45	694.5	37.1	342	AAW81576	AAW81576 EBV-induc

ALIGNMENTS

RESULT 1	AA45039	standard; protein; 358 AA.
XX	AA45039;	
XX	31-MAY-2000	(first entry)
XX	Human G protein-coupled receptor, HG03.	
DE	HG03; G protein-coupled receptor; GPCR; screen; agonist; antagonist;	
KW	pharmaceutical; gene therapy; human.	
KM		
OS	Homo sapiens.	
XX	WO200008133-A1.	
PN	17-FEB-2000.	
PD	02-AUG-1999;	99WO-US017388.
PF	02-AUG-1999;	99WO-US017388.
XX	06-AUG-1998;	98US-0095571P.
PR	(MERI) MERCK & CO INC.	
XX	Liu Q, McDonald TP, Wang R;	
PI	WPI; 2000-205701/18.	
DR	N-PSDB; AA250776.	
XX	Novel G-protein coupled receptor cDNA molecule encoding HG03 polypeptide	
PT	useful for identifying its agonists and antagonists which are useful in	
PT	pharmaceuticals.	
XX	Claim 1; Fig 2; 36pp; English.	
PS	The present sequence is human HG03 protein, which is a G protein-coupled	
CC	receptor (GPCR). It shows homology to human platelet activating factor	
CC	receptor (GPR). It is expressed at high levels in prostate, placenta and	
CC	trachea and at low levels in thymus and testis. HG03 expression vectors	
CC	can be used to transform host cells, which may be used in screening for	
CC	agonists or antagonists that are potential pharmaceuticals. It can be	
CC	used in gene therapy for treatment of diseases associated with low HG03	
CC	activity	
XX	Sequence 358 AA;	
SO	Query Match	100.0%; Score 1874; DB 3; Length 358;

Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGPNLTAKLPNNELHGOESHNSGNSDGPDKNTTIANEPDTIVLPVLYLIIFVASILLN 60
XX |||||||
CC 1 MGPNLTAKLPNNELHGOESHNSGNSDGPDKNTTIANEPDTIVLPVLYLIIFVASILLN 60
CC is expressed in prostate, uterus and placenta and participates in
CC signalling pathway. The receptor polypeptide is useful in drug screening
CC assays, and to identify modulating agents. Epitope bearing peptides are
CC used to raise specific antibodies. The polypeptide and modulating agents
CC can also be used for the modulation, diagnosis or treatment of immune or
CC respiratory disorders, e.g. Crohn's disease, multiple sclerosis, asthma,
CC allergies, viral, bacterial or parasitic infections, cystic fibrosis,
CC pneumonia, Legionnaires disease or sinusitis
DB 121 FYANNMTSIVFGLISIDRYLKVKVPFGDSRMYSITFPKVLSCVWVIMAVLSLPIIILT 180
QY 121 FYANNMTSIVFGLISIDRYLKVKVPFGDSRMYSITFPKVLSCVWVIMAVLSLPIIILT 180
DB 181 NGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFVAVLVILIGCYIAISRYIHKSSROF 240
QY 241 ISQSRKRRKQNSIRVVAVVFTCFPLPYHLCRIPFTFSHLDRLLDESAOKILYYCKEITL 300
DB 241 ISQSRKRRKQNSIRVVAVVFTCFPLPYHLCRIPFTFSHLDRLLDESAOKILYYCKEITL 300
QY 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSEVRITYYDTDV 358
DB 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSEVRITYYDTDV 358

```

RESULT 2

AAV44365
ID AAV44365 standard; protein; 358 AA.

XX AAV44365;
DT 14-MAR-2000 (first entry)

DE Human G-protein coupled 2871 receptor protein.

XX GPCR; G-protein coupled receptor; signalling pathway;
KW drug screening assay; immune disorder; respiratory disorder;
KW Crohn's disease; multiple sclerosis; asthma; allergy; viral infection;
KW bacterial infection; parasitic infection; cystic fibrosis; pneumonia;
KW Legionnaires disease; sinusitis.

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers

FT Domain 1..42 /label= Extracellular_domain

FT Domain 43..318 /label= Transmembrane_domain

FT Region 138..140 /note="GPCR signal transduction signature"

FT Domain 319..359 /label= Intracellular_domain

XX WO963087-A1.

XX 09-DEC-1999.

XX 02-JUN-1999; 99WO-US012203.

XX 02-JUN-1999; 98US-00088857.

XX (MILL-) MILLENNIUM PHARM INC.

XX Glucksmann MA, Hodg MR;

XX WPI; 2000-105698/09.

XX N-PSDB; AA229524.

PT Isolated human nucleic acid encoding a novel G-protein coupled receptor
useful for the modulation, diagnosis or treatment of immune or

PT respiratory disorders.

XX Claim 1; Fig 1; 79pp; English.

CC The present sequence is G-protein coupled receptor designated 2871. This
CC is expressed in prostate, uterus and placenta and participates in
CC signalling pathway. The receptor polypeptide is useful in drug screening
CC assays, and to identify modulating agents. Epitope bearing peptides are
CC used to raise specific antibodies. The polypeptide and modulating agents
CC can also be used for the modulation, diagnosis or treatment of immune or
CC respiratory disorders, e.g. Crohn's disease, multiple sclerosis, asthma,
CC allergies, viral, bacterial or parasitic infections, cystic fibrosis,
CC pneumonia, Legionnaires disease or sinusitis

XX Sequence 358 AA;

QY Query Match 100.0%; Score 1874; DB 3; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGPNLTAKLPNNELHGOESHNSGNSDGPDKNTTIANEPDTIVLPVLYLIIFVASILLN 60
DB 1 MGPNLTAKLPNNELHGOESHNSGNSDGPDKNTTIANEPDTIVLPVLYLIIFVASILLN 60
QY 61 GLAVWIFPHIRNKTSFIYFLKNIVVADLIMTLTPFPRIVHDAGFGPMWFKFLCKRTSVL 120
DB 61 GLAVWIFPHIRNKTSFIYFLKNIVVADLIMTLTPFPRIVHDAGFGPMWFKFLCKRTSVL 120
QY 121 FYANNMTSIVFGLISIDRYLKVKVPFGDSRMYSITFPKVLSCVWVIMAVLSLPIIILT 180
DB 121 FYANNMTSIVFGLISIDRYLKVKVPFGDSRMYSITFPKVLSCVWVIMAVLSLPIIILT 180
QY 181 NGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFVAVLVILIGCYIAISRYIHKSSROF 240
DB 181 NGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFVAVLVILIGCYIAISRYIHKSSROF 240
QY 241 ISQSRKRRKQNSIRVVAVVFTCFPLPYHLCRIPFTFSHLDRLLDESAOKILYYCKEITL 300
DB 241 ISQSRKRRKQNSIRVVAVVFTCFPLPYHLCRIPFTFSHLDRLLDESAOKILYYCKEITL 300
QY 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSEVRITYYDTDV 358
DB 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSEVRITYYDTDV 358

```

RESULT 3

AAAB83014
ID AAB83014 standard; protein; 358 AA.

XX AAB83014;

XX 22-JUN-2001 (first entry)

DE Human G protein coupled receptor HOKR2.

XX Human; HOKR2; G protein coupled receptor; antiinflammatory; antiallergic;
KW immune disease; inflammatory disease; bronchitis; allergy.

XX Homo sapiens.

XX JP2001029084-A.

XX 06-FEB-2001.

XX 23-JUL-1999; 99JP-00209919.

XX 23-JUL-1999; 99JP-00209919.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX WPI; 2001-303765/32.

XX N-PSDB; AAF82359.

PT Novel G protein coupled receptor, and a gene of the G protein coupled
PT receptor, useful for screening for agents to prevent and treat
PT inflammatory diseases such as bronchitis.

PS Claim 1; Page 10-11; 13pp; Japanese.

CC The present sequence is a novel human G protein coupled receptor
CC designated HORK2. The total length HORK2 cDNA was obtained by reverse
CC transcription-polymerase chain reaction (RT-PCR) using human spleen-
CC derived mRNA as the template. The G protein coupled receptor may be used
CC to screen for agents that are useful in the prevention and treatment of
CC immune diseases and inflammatory diseases such as bronchitis and allergy

XX Sequence 358 AA;

Query Match 100.0%; Score 1874; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPNITLAKLPNNELHGOESHNSGNSDGPCKNTLHNEPDTIVLPVLYLIFVASILLN 60
DB 1 MGPNITLAKLPNNELHGOESHNSGNSDGPCKNTLHNEPDTIVLPVLYLIFVASILLN 60
QY 61 GLAVWIFPHIRNKTSFIYLNKIVVADLIMLTLPFRIVHDAGFGPMYFKFLCKRYTSVL 120
DB 61 GLAVWIFPHIRNKTSFIYLNKIVVADLIMLTLPFRIVHDAGFGPMYFKFLCKRYTSVL 120
QY 121 FYANNYTSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
DB 121 FYANNYTSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
QY 181 NGQPTEDNIHDSCKLSPGVKMTAVTVVNSCLFVAVALVILIGCYIAISRYIHKSHPF 240
DB 181 NGQPTEDNIHDSCKLSPGVKMTAVTVVNSCLFVAVALVILIGCYIAISRYIHKSHPF 240
QY 241 ISQSRKKKHNSIRVVAVVFTCPPLPYHLCRIPFTFSLDLRLDESQKILYCKEITL 300
DB 241 ISQSRKKKHNSIRVVAVVFTCPPLPYHLCRIPFTFSLDLRLDESQKILYCKEITL 300
QY 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQSVRSEVRYYDYTDV 358
DB 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQSVRSEVRYYDYTDV 358

RESULT 4

AAB96884 ID AAB96884 standard; protein; 358 AA.

XX AAB96884;

XX 13-JUL-2001 (first entry)

XX Human novel G-protein coupled receptor.

XX Human; G-protein coupled receptor; disease screening; immune disease;

XX inflammatory disease; bronchitis; allergy.

XX Homo sapiens.

XX JP2001054388-A.

XX 27-FEB-2001.

XX 17-AUG-1999; 99JP-00230776.

XX 17-AUG-1999; 99JP-00230776.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX WPI; 2001-321038/34.

XX N-PSDB; AAF86985.

XX A new G protein coupled receptor and G protein coupled receptor gene.

XX Claim 1; Page 10-11; 14pp; Japanese.

CC The present invention provides the protein and coding sequences of a
CC novel human G-protein coupled receptor. This is useful as a screening
CC tool for preventive and treatment agents of immune inflammatory diseases
CC such as bronchitis and allergies. The present sequence is the protein of
CC the invention

XX Sequence 358 AA;

Query Match 100.0%; Score 1874; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPNITLAKLPNNELHGOESHNSGNSDGPCKNTLHNEPDTIVLPVLYLIFVASILLN 60
DB 1 MGPNITLAKLPNNELHGOESHNSGNSDGPCKNTLHNEPDTIVLPVLYLIFVASILLN 60
QY 61 GLAVWIFPHIRNKTSFIYLNKIVVADLIMLTLPFRIVHDAGFGPMYFKFLCKRYTSVL 120
DB 61 GLAVWIFPHIRNKTSFIYLNKIVVADLIMLTLPFRIVHDAGFGPMYFKFLCKRYTSVL 120
QY 121 FYANNYTSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
DB 121 FYANNYTSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
QY 181 NGQPTEDNIHDSCKLSPGVKMTAVTVVNSCLFVAVALVILIGCYIAISRYIHKSHPF 240
DB 181 NGQPTEDNIHDSCKLSPGVKMTAVTVVNSCLFVAVALVILIGCYIAISRYIHKSHPF 240
QY 241 ISQSRKKKHNSIRVVAVVFTCPPLPYHLCRIPFTFSLDLRLDESQKILYCKEITL 300
DB 241 ISQSRKKKHNSIRVVAVVFTCPPLPYHLCRIPFTFSLDLRLDESQKILYCKEITL 300
QY 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQSVRSEVRYYDYTDV 358
DB 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQSVRSEVRYYDYTDV 358

RESULT 5

AAB03199 ID AAB03199 standard; protein; 358 AA.

XX AAB03199;

XX 03-AUG-2001 (first entry)

XX Human G-protein coupled receptor 287L.

XX Human; G-protein coupled receptor; 287L receptor; therapy;
XX immune disorder; respiratory disorder; haematopoietic disorder;
XX bone marrow disorder; brain disorder; heart disorder; kidney disorder;
XX blood vessel disorder; prostate disorder; skeletal muscle disorder;
XX ovary disorder; epidiymis disorder; spleen disorder; liver disorder;
XX T-cells related-disorder; thymus related-disorder; breast disorder;
XX B cells related-disorder; thyroid disorder; pancreas disorder;
XX precursor T cell neoplasm related-disorder; antineoplastic;
XX anti-diabetic; antiallergic; antileukemic; antiviral; ophthalmological;
XX antibacterial; antihelminthic; antiparasitic; antifungal; cytostatic;
XX antihemorrhagic; neuroprotective; nootropic; antirheumatic; vasotropic;
XX hepatotropic; immunosuppressive; angiogenic; hypotensive; cardiac;
XX antiarteriosclerotic; nephrotropic; virostatic; thrombolytic; haemostatic;
XX human immunodeficiency virus; anti-HIV; dermatological; thyromimetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 1..42

XX Domain 43..318

XX Region 138..140

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FT      Domain /label= GPCR_signal_transduction_signature
FT      319..358 /label= Intracellular_domain
XX      MO200144474-A1.
XX      21-JUN-2001.
PD      18-DEC-2000; 2000MO-US035004.
PF      16-DEC-1999; 99US-00464685.
PR      (MILL-) MILLENNIUM PHARM INC.
XX      Glucksmann MA, Hodge MR, Hunter JJ, Rudolph-Owen L, Welch NS;
XX      MPI, 2001-390250/41.
XX      N-PSDB; AAD06915.
XX      Identifying inhibitors or modulators of novel protein, 2871 receptor, a G
XX      protein coupled receptor, useful for treating Crohn's disease, insulin
XX      dependent diabetes mellitus, multiple sclerosis, bronchial asthma.
XX      Claim 1, Fig 1A-ID; 107pp; English.
XX      The present sequence is a human G-protein coupled receptor, 2871
XX      receptor. The 2871 receptor is used for screening a compound that acts as
XX      agonist and antagonist to 2871 receptor. The compounds can be used for
XX      treating disorders such as immune disorders (e.g., asthma and glomerular
XX      nephritis), respiratory disorders (e.g., bronchitis and cystic fibrosis),
XX      haematopoietic disorders involving cells of leukocyte, erythrocyte and
XX      platelet lineages, bone marrow disorders (e.g., leukaemias and lymphoma),
XX      brain disorders (e.g., intracranial haemorrhage, acute meningitis,
XX      multiple sclerosis and Alzheimer's disease), heart disorders (e.g.,
XX      rheumatic heart disease, angina pectoris and myocardial infarction),
XX      blood vessel disorders (e.g., atherosclerosis and hypertension), kidney
XX      disorders (e.g., autosomal recessive polycystic kidney disease, acquired
XX      cystic disease and Heymann nephritis), prostate disorders (e.g., nodular
XX      hyperplasia and carcinoma), skeletal muscle disorders (e.g.,
XX      rhabdomyosarcoma), ovary disorders (e.g., ovarian tumour,
XX      cystadenofibroma), testis and epididymis disorders (e.g., gonorrhoea,
XX      mumps and syphilis), spleen disorders (e.g., congestive splenomegaly and
XX      congenital anomalies), liver disorders (e.g., autoimmune hepatitis and
XX      cirrhosis), T-cells related-disorders (e.g., acquired immunodeficiency
XX      syndrome (AIDS) and inflammatory myopathies), thymus related-disorders
XX      (e.g., thymic cysts and germ cell tumours), B cells related-disorders
XX      (e.g., follicular lymphoma and multiple myeloma), breast related-
XX      disorders (e.g., fat necrosis and fibrocystic changes), thyroid disorders
XX      (e.g., cretinism and myxedema), pancreas disorders (e.g., pancreatitis
XX      and diabetes mellitus) and precursor T cell neoplasm related-disorders
XX      (e.g., T-cell chronic lymphocytic leukaemia)
XX      Sequence 358 AA;
SQ

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```

Query Match      100.0%; Score 1874; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MGFNLTAKLNNELHGOESHNSGNRSGDKNTLHNEFDITVAPVYLITFVASITLNN 60
DB      1 MGFNLTAKLNNELHGOESHNSGNRSGDKNTLHNEFDITVAPVYLITFVASITLNN 60
QY      61 GLAWVIFHIRKNTSFIYFLKNIIVADLIMTLTPPRIVHDAGFPWYFKFLCYRTSVL 120
DB      61 GLAWVIFHIRKNTSFIYFLKNIIVADLIMTLTPPRIVHDAGFPWYFKFLCYRTSVL 120
QY      121 FYANNYTSIVFLGLISIDRYLKVVRPFQDSRMYSITTFKVLSCVQWIMAVLSLNNIIT 180
DB      121 FYANNYTSIVFLGLISIDRYLKVVRPFQDSRMYSITTFKVLSCVQWIMAVLSLNNIIT 180
QY      181 NGQPTEDNINHDSKSLKSPGVKMTAVNYVNSCLFVAVYVILIGCYIASRIYHSSRPF 240
DB      181 NGQPTEDNINHDSKSLKSPGVKMTAVNYVNSCLFVAVYVILIGCYIASRIYHSSRPF 240

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QY      241 ISOSRKRKHNSIRVWVAVPTCELPYHICRIPTFSHLDRLLDESOKILYYCKEITL 300
DB      241 ISOSRKRKHNSIRVWVAVPTCELPYHICRIPTFSHLDRLLDESOKILYYCKEITL 300
QY      301 FLACNVCLDPIIYFPCRSFGRRLFKKSNIRTSSESIRLSQSVARSEVRITYDYTDV 358
DB      301 FLACNVCLDPIIYFPCRSFGRRLFKKSNIRTSSESIRLSQSVARSEVRITYDYTDV 358

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RESULT 6
AAE67484
ID AAE67484 standard; protein; 358 AA.
XX
AC AAE67484;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a human octoray polypeptide.
XX
KW Human; octoray; G-protein coupled receptor; infection; pain; cancer;
KW diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease;
KW acute heart failure; hypotension; hypertension; urinary retention;
KW osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer;
KW allergy; benign prostatic hypertrophy; migraine; vomiting;
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW manic depression; depression; delirium; dementia; mental retardation;
KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome.
XX
OS Homo sapiens.
XX
PN WO200109166-A1.
XX
PD 08-FEB-2001.
XX
PF 21-JUL-2000; 2000MO-US020005.
XX
PR 29-JUL-1999; 99US-00363203.
XX
PA (SMK ) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Eishourbagy NA, Guerrero SF, Gattu N, Mooney JT,
PI Vawter L;
XX
DR MPI; 2001-182933/18.
XX
DR N-PSDB; AAF55101.
XX

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XX      Novel octoray polypeptides and polynucleotides encoding a G-protein
XX      coupled receptor for diagnosis and treatment of bacterial infections,
XX      cancer, neurological disorders, obesity and for identifying agonists and
XX      antagonists.
XX
PS      Claim 1; Page 27-28; 31pp; English.
XX

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XX      The present sequence represents a human octoray polypeptide. Octoray is a
XX      member of the G-protein coupled receptor family. Octoray polypeptides,
XX      CC polynucleotides and antibodies are useful for diagnosis and treatment of
XX      certain diseases, including bacterial, fungal, protozoan and viral
XX      infections, particularly infections caused by HIV-1 and HIV-2, pain,
XX      cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's
XX      disease, acute heart failure, hypotension, hypertension, urinary
XX      retention, osteoporosis, angina pectoris, myocardial infarction, stroke,
XX      ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting,
XX      psychotic and neurological disorders, including anxiety, schizophrenia,
XX      manic depression, depression, delirium, dementia, and severe mental
XX      retardation, dyskinesia, such as Huntington's disease or Gilles de la
XX      Tourette's syndrome
XX
SQ      Sequence 358 AA;

```

```

Query Match      100.0%; Score 1874; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGFNLTAKLPNNELHGOESHNSGRSDPGKNTTLHNEPPTIVLPVYLIIFVASILLN 60
 DB 1 MGFNLTAKLPNNELHGOESHNSGRSDPGKNTTLHNEPPTIVLPVYLIIFVASILLN 60
 QY 61 GLAWIFPHIRNKTSFIYLNKNIIVADLIMLTPEPFRIVHDAGFGPMWFKPILCRYSVL 120
 DB 61 GLAWIFPHIRNKTSFIYLNKNIIVADLIMLTPEPFRIVHDAGFGPMWFKPILCRYSVL 120
 QY 121 FYANNYTSIVFLGLISIDRYLKVVKPFQDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 DB 121 FYANNYTSIVFLGLISIDRYLKVVKPFQDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 QY 181 NGOPTEDNIHDCSKLSPGLGKMTAVTVVNSCLFVAVLVLLIGCYIAISRIRHSSROF 240
 DB 181 NGOPTEDNIHDCSKLSPGLGKMTAVTVVNSCLFVAVLVLLIGCYIAISRIRHSSROF 240
 QY 241 ISQSRKXKXNQSIRVVAVVFTCPFLPYHLGRIPFTFPHLDRLDESAOKILYYCKEITL 300
 DB 241 ISQSRKXKXNQSIRVVAVVFTCPFLPYHLGRIPFTFPHLDRLDESAOKILYYCKEITL 300
 QY 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTRSESIRLSQSVRSEVRYYDYTDV 358
 DB 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTRSESIRLSQSVRSEVRYYDYTDV 358

RESULT 7
 ABR48208
 ID ABR48208 standard; protein, 358 AA.
 XX ABR48208;
 AC ABR48208;
 DT 12-JUN-2003 (first entry)
 XX Human bladder cancer associated protein sequence SEQ ID NO:135.
 XX Human bladder cancer; cytostatic; gene therapy; vaccine.
 XX Homo sapiens.
 XX MO2003003906-A2.
 PD 16-JAN-2003.
 XX 03-JUL-2002; 2002WO-US021338.
 XX 03-JUL-2001; 2001US-0302814P.
 PR 03-AUG-2001; 2001US-0310099P.
 PR 08-NOV-2001; 2001US-0343705P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 12-APR-2002; 2002US-0372246P.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Mack DH, Aziz N;
 XX WPI; 2003-201532/19.
 DR N-PSDB; ACC51022.
 XX Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.
 XX Claim 10; Page 277; 307pp; English.
 PS The present invention describes a method for detecting a bladder cancer-
 XX associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridizes to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059).
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and

CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications

SO Sequence 358 AA;

Query Match 100.0%; Score 1874; DB 6; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.6e-204;
 Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFNLTAKLPNNELHGOESHNSGRSDPGKNTTLHNEPPTIVLPVYLIIFVASILLN 60
 DB 1 MGFNLTAKLPNNELHGOESHNSGRSDPGKNTTLHNEPPTIVLPVYLIIFVASILLN 60
 QY 61 GLAWIFPHIRNKTSFIYLNKNIIVADLIMLTPEPFRIVHDAGFGPMWFKPILCRYSVL 120
 DB 61 GLAWIFPHIRNKTSFIYLNKNIIVADLIMLTPEPFRIVHDAGFGPMWFKPILCRYSVL 120
 QY 121 FYANNYTSIVFLGLISIDRYLKVVKPFQDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 DB 121 FYANNYTSIVFLGLISIDRYLKVVKPFQDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 QY 181 NGOPTEDNIHDCSKLSPGLGKMTAVTVVNSCLFVAVLVLLIGCYIAISRIRHSSROF 240
 DB 181 NGOPTEDNIHDCSKLSPGLGKMTAVTVVNSCLFVAVLVLLIGCYIAISRIRHSSROF 240
 QY 241 ISQSRKXKXNQSIRVVAVVFTCPFLPYHLGRIPFTFPHLDRLDESAOKILYYCKEITL 300
 DB 241 ISQSRKXKXNQSIRVVAVVFTCPFLPYHLGRIPFTFPHLDRLDESAOKILYYCKEITL 300
 QY 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTRSESIRLSQSVRSEVRYYDYTDV 358
 DB 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTRSESIRLSQSVRSEVRYYDYTDV 358

RESULT 8
 ABUS6683
 ID ABUS6683 standard; protein, 358 AA.
 XX ABUS6683;
 AC ABUS6683;
 DT 02-APR-2003 (first entry)
 XX Lung cancer-associated polypeptide #276.
 XX Lung cancer-associated polypeptide #276.
 XX Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX Unidentified.
 OS Unidentified.
 XX MO200286443-A2.
 PD 31-OCT-2002.
 XX 18-APR-2002; 2002WO-US012476.
 XX 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0230492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Mack DH, Murray R;
 XX Aziz N, Murray R;

XX MPI: 2003-093161/08.
DR N-PSDB; ABX76412.
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer.
XX
PS Claim 27; Page 400; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
CC invention
XX
SQ Sequence 358 AA;
XX
Query Match 100.0%; Score 1874; DB 6; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MGFNLTTLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEFTIVLPVLYLIIFVASIILN 60
DB 1 MGFNLTTLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEFTIVLPVLYLIIFVASIILN 60
XX
QY 61 GLAVWIFPHIRNKTSFIPLYKNIVADLIMTLTPFPRIYHDAGFGPMYFKFLCRYTSVL 120
DB 61 GLAVWIFPHIRNKTSFIPLYKNIVADLIMTLTPFPRIYHDAGFGPMYFKFLCRYTSVL 120
XX
QY 121 FYANMYTSIVELGLISIDRYLKVKRPGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
DB 121 FYANMYTSIVELGLISIDRYLKVKRPGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
XX
QY 181 NGOPTEDNIDHCSKLKSPGLGVMKHTAVTYNSCLFVAVVILIGCYIAISRTHKSSROF 240
DB 181 NGOPTEDNIDHCSKLKSPGLGVMKHTAVTYNSCLFVAVVILIGCYIAISRTHKSSROF 240
XX
QY 241 ISOSRRKRKKNOSIRVVAVVFTFCFLPYHLCRIPTFTSHLDRLDLSAOKILVYCKEITL 300
DB 241 ISOSRRKRKKNOSIRVVAVVFTFCFLPYHLCRIPTFTSHLDRLDLSAOKILVYCKEITL 300
XX
QY 301 FLASACNVCLDPIITYFPMCRSFSRRLFKKSNIRTRSESIRLSQVRSREVRYYDYTDV 358
DB 301 FLASACNVCLDPIITYFPMCRSFSRRLFKKSNIRTRSESIRLSQVRSREVRYYDYTDV 358
XX
RESULT 9
ABR01795
ID ABR01795 standard; protein; 358 AA.
XX
AC ABR01795;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein, 154P2A8.
XX
KW Human; cytosolic; vaccine; cancer; immune response.

XX Homo sapiens.
OS
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
XX
XX 10-APR-2001; 2001US-0283112P.
XX
XX 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Farris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX
XX MPI: 2003-075555/07.
XX
XX N-PSDB; ABZ78126.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response in
XX cancer patients.
XX
XX Claim 12; Fig 2F, 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer
XX
SQ Sequence 358 AA;
XX
Query Match 100.0%; Score 1874; DB 6; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MGFNLTTLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEFTIVLPVLYLIIFVASIILN 60
DB 1 MGFNLTTLAKLPNNELHGOESHNSGNRSDGPKNTTLHNEFTIVLPVLYLIIFVASIILN 60
XX
QY 61 GLAVWIFPHIRNKTSFIPLYKNIVADLIMTLTPFPRIYHDAGFGPMYFKFLCRYTSVL 120
DB 61 GLAVWIFPHIRNKTSFIPLYKNIVADLIMTLTPFPRIYHDAGFGPMYFKFLCRYTSVL 120
XX
QY 121 FYANMYTSIVELGLISIDRYLKVKRPGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
DB 121 FYANMYTSIVELGLISIDRYLKVKRPGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
XX
QY 181 NGOPTEDNIDHCSKLKSPGLGVMKHTAVTYNSCLFVAVVILIGCYIAISRTHKSSROF 240
DB 181 NGOPTEDNIDHCSKLKSPGLGVMKHTAVTYNSCLFVAVVILIGCYIAISRTHKSSROF 240
XX
QY 241 ISOSRRKRKKNOSIRVVAVVFTFCFLPYHLCRIPTFTSHLDRLDLSAOKILVYCKEITL 300
DB 241 ISOSRRKRKKNOSIRVVAVVFTFCFLPYHLCRIPTFTSHLDRLDLSAOKILVYCKEITL 300
XX
QY 301 FLASACNVCLDPIITYFPMCRSFSRRLFKKSNIRTRSESIRLSQVRSREVRYYDYTDV 358
DB 301 FLASACNVCLDPIITYFPMCRSFSRRLFKKSNIRTRSESIRLSQVRSREVRYYDYTDV 358
XX
RESULT 10
ABP81966
ID ABP81966 standard; protein; 358 AA.

XX AC ABP81966;
 XX DT 04-MAR-2003 (first entry)
 XX DE Human G protein-coupled receptor GPR87/95 protein SEQ ID NO:418.
 XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor; modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX OS Homo sapiens.
 XX PN WO200261087-A2.
 XX PD 08-AUG-2002.
 XX PF 19-DEC-2001; 2001WO-US050107.
 XX PR 19-DEC-2000; 2000US-0257144P.
 XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX PI Bumer GC, Roush CL, Brown JP;
 XX DR WPI; 2003-046718/04.
 XX DR N-PSDB; AB242814.
 XX PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR) useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX PS Disclosure; Fig 1; 523pp; English.
 XX CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnoses. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX SO Sequence 358 AA;

Query Match 100.0%; Score 1874; DB 6; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.6e-204;

Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGPNLTAKLPNNELHGESHNNGRSDGPKNTLNHEPPTIVLPUYLIIIVASILLN 60
 DB 1 MGPNLTAKLPNNELHGESHNNGRSDGPKNTLNHEPPTIVLPUYLIIIVASILLN 60
 QY 61 GLAWIFPHIRNKTSPIFYLNKIVADIMLTLPFRIIVHDAGFGPMYEFKFLCRYSVL 120
 DB 61 GLAWIFPHIRNKTSPIFYLNKIVADIMLTLPFRIIVHDAGFGPMYEFKFLCRYSVL 120
 QY 121 FYANMTYSIVELGISIDRYLKVKRPFCDSSMYSTFTKVLSCVWVIMAVLSLNNILT 180
 DB 121 FYANMTYSIVELGISIDRYLKVKRPFCDSSMYSTFTKVLSCVWVIMAVLSLNNILT 180
 QY 181 NGQPTEDNIHCSLKLSPGKRVKHTAVTYVNSCLPVALVYLIGYIAISRIYKSSQF 240
 DB 181 NGQPTEDNIHCSLKLSPGKRVKHTAVTYVNSCLPVALVYLIGYIAISRIYKSSQF 240
 QY 241 ISOSRRKKNQSRVVAVVFTCELPYHLGRIPFTFSLRLDSDSAQKILYCKEITL 300
 DB 241 ISOSRRKKNQSRVVAVVFTCELPYHLGRIPFTFSLRLDSDSAQKILYCKEITL 300
 QY 301 FLACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQSVRRSEVRYYDYTDV 358
 DB 301 FLACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQSVRRSEVRYYDYTDV 358
 RESULT 11
 ID ABU09897 standard; protein, 358 AA.
 XX AC ABU09897;
 XX DT 11-AUG-2003 (first entry)
 XX DE Human G-protein coupled receptor 2871.
 KW Human; receptor; G-protein coupled receptor; gene therapy; pneumonia;
 KW immune disorder; Crohn's disease; Grave's disease; respiratory disorder;
 KW diphtheria; haematopoietic disorder; leukaemia; systemic sclerosis;
 KW prostatic disorder; benign prostate hypertrophy; tumour; breast disease;
 KW acute mastitis; Paget's disease; muscular disorder; rhabdomyosarcoma;
 KW neurological disorder; cerebral oedema; Parkinson's disease; atrophy;
 KW blood vessel disorder; atherosclerosis; testicular disease; syphilis;
 KW epididymal disease; thyroid disease; hyperthyroidism; cretinism; AIDS;
 KW kidney disorder; cystic renal dysplasia; glomerulonephritis;
 KW cardiovascular disease; heart failure; pericarditis; pancreatic disease;
 KW pancreatitis; diabetes mellitus; chymus disease; thymic hypoplasia;
 KW Hodgkin disease; spleen disease; splenomegaly; Gaucher disease;
 KW liver disease; hepatic failure; alcoholic liver disease; T-cell disorder;
 KW systemic lupus erythematosus; B-cell disorder; Burkitt lymphoma;
 KW multiple myeloma; platelet disorder; thrombocytopenia;
 KW haemolytic-uraemic syndrome.
 OS Homo sapiens.
 PN US2003017539-A1.
 PD 23-JAN-2003.
 PF 07-JUN-2002; 2002US-00165844.
 PR 02-JUN-1998; 98US-00088857.
 PR 02-SEP-1998; 98US-00145745.
 PR 21-JAN-1999; 99US-00234923.
 PR 02-JUN-1999; 99US-00324465.
 PR 28-JUN-1999; 99US-00340880.
 PR 26-AUG-1999; 99US-00383745.
 PR 16-DEC-1999; 99US-00464685.
 PR 18-DEC-2000; 2000US-007411783.
 PA (MILL-) MILLENNIUM PHARM INC.


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Db      241  ISGSRKRNQSIIRVVAVFTGFLPYHLCRIFPTFPHDLRLDESAOKILYYCKEITL 300
Qy      301  FLACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRSLQSVRRSEVRRIYYDTDV 358
Db      301  FLACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRSLQSVRRSEVRRIYYDTDV 358

RESULT 13
AAE34534 ID AAE34534 standard; protein; 366 AA.
AC AAE34534;
DE 14-MAY-2003 (first entry)
DE Human Mowgli G-protein coupled receptor with FLAG tag.
XX
XX Mowgli G-protein coupled receptor; GPCR; immune response; infection;
XX neurological disorder; Parkinson's disease; obesity; asthma; cancer;
XX anorexia; pain; diabetes; vaccine; human.
XX Homo sapiens.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Region 1..358
XX FT /note= "Human Mowgli GPCR protein"
XX FT 359..366
XX FT /note= "FLAG tag"
XX
XX WO200292624-A2.
XX
XX 21-NOV-2002.
XX
XX 16-MAY-2002; 2002WO-GB002304.
XX
XX 16-MAY-2001; 2001GB-00011959.
XX 18-MAY-2001; 2001US-0292141P.
XX
XX (PARA-) PARADIGM THERAPEUTICS LTD.
XX
XX Carleton M, Aparicio S, Dixon J, Thresher R, Zahn D;
XX WPI; 2003-129261/12.
XX
XX New Mowgli G-protein coupled receptor polypeptides and polynucleotides,
XX useful for inducing immunological response to produce antibody and/or T
XX cell immune response against e.g. bacterial, fungal, protozoan or viral
XX infections.
XX
XX Claim 1; Page 117-118; 121pp; English.
XX
XX The invention relates to novel Mowgli G-protein coupled receptor (GPCR)
XX polypeptides and polynucleotides. Mowgli polypeptides, nucleic acids,
XX probes, antibodies, expression vectors and ligands are useful as
XX biosensors, for detection, diagnosis, or treatment of diseases associated
XX with over-, under- or abnormal expression of Mowgli GPCR in tissues, in
XX genetic analysis and in chromosome identification. Polypeptides of the
XX invention may be used for screening compounds which bind the receptor and
XX which activate (agonists) or inhibit (antagonists) activation of Mowgli.
XX They may further be used as vaccines to induce immunological response to
XX produce antibody and/or T cell immune response against e.g. bacterial,
XX protozoan, fungal or viral infections, pain, cancers, diabetes, obesity,
XX anorexia, asthma, Parkinson's disease and other neurological disorders.
XX The present sequence is human Mowgli G-protein coupled receptor with FLAG
XX tag
XX
XX Sequence 366 AA;
XX
Query Match 100.0%; Score 1874; DB 6; Length 366;
Best Local Similarity 100.0%; Pred. No. 6,8e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MGRVLTLAKLPPNNELHGOESNNSGNSRSDGPKGKNTLHNEPPTIVLPVLYLIIPVASILLN 60
Db      1  MGRVLTLAKLPNNELHGOESNNSGNSRSDGPKGKNTLHNEPPTIVLPVLYLIIPVASILLN 60
Qy      61  GLAWIFPHIRNKTSFIIFYLNIVADLIMTLTFFPRIVHDAGCGPWYFEKILCRYTVL 120
Db      61  GLAWIFPHIRNKTSFIIFYLNIVADLIMTLTFFPRIVHDAGCGPWYFEKILCRYTVL 120
Qy      121  FYANNVTSIVFLGISIDRYLKVKVPFGDSNMYSTITFTKVLSCVWVIMAVLSLPIIILT 180
Db      121  FYANNVTSIVFLGLISIDRYLKVKVPFGDSNMYSTITFTKVLSCVWVIMAVLSLPIIILT 180
Qy      181  NGQPTEDNIDHCSLKSPLGVKMHAVTVNSCLFVAVLVILGCIYIAISRHHKSRQF 240
Db      181  NGQPTEDNIDHCSLKSPLGVKMHAVTVNSCLFVAVLVILGCIYIAISRHHKSRQF 240
Qy      241  ISGSRKRNQSIIRVVAVFTGFLPYHLCRIFPTFPHDLRLDESAOKILYYCKEITL 300
Db      241  ISGSRKRNQSIIRVVAVFTGFLPYHLCRIFPTFPHDLRLDESAOKILYYCKEITL 300
Qy      301  FLACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRSLQSVRRSEVRRIYYDTDV 358
Db      301  FLACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRSLQSVRRSEVRRIYYDTDV 358

RESULT 14
AAE34533 ID AAE34533 standard; protein; 364 AA.
AC AAE34533;
DE 14-MAY-2003 (first entry)
DE Human Mowgli G-protein coupled receptor with V5 and His tag.
XX
XX Mowgli G-protein coupled receptor; GPCR; immune response; infection;
XX neurological disorder; Parkinson's disease; obesity; asthma; cancer;
XX anorexia; pain; diabetes; vaccine; human.
XX Homo sapiens.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Region 1..364
XX FT /note= "Human Mowgli GPCR protein"
XX FT 365..378
XX FT /note= "V5 tag"
XX FT 379..384
XX FT /note= "His tag"
XX
XX WO200292624-A2.
XX
XX 21-NOV-2002.
XX
XX 16-MAY-2002; 2002WO-GB002304.
XX
XX 16-MAY-2001; 2001GB-00011959.
XX 18-MAY-2001; 2001US-0292141P.
XX
XX (PARA-) PARADIGM THERAPEUTICS LTD.
XX
XX Carleton M, Aparicio S, Dixon J, Thresher R, Zahn D;
XX WPI; 2003-129261/12.
XX
XX New Mowgli G-protein coupled receptor polypeptides and polynucleotides,
XX useful for inducing immunological response to produce antibody and/or T
XX cell immune response against e.g. bacterial, fungal, protozoan or viral
XX infections.
XX
XX Claim 1; Page 117; 121pp; English.
XX

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